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                                        GenCore version 5.1.3
                          Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:           October 17, 2002, 15:20:12 ; Search time 8.55049 Seconds
                                              (without alignments)
                                              357.079 Million cell updates/sec

Title:            US-10-018-924-2_COPY_22_146
Perfect score:    655
Sequence:         1 ARLDVASEFRKKWNKWALSR.........FTDKDKDNVAPRSKISPQGY 125

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:      231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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                    %       Query
Result             Match    Length  DB
No.      Score     Match    Length  DB   ID                    Description
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  1       655      100.0    185     1    US-08-233-389C-1       Sequence 1, Appli
  2       655      100.0    185     2    US-08-801-863-1        Sequence 1, Appli
  3       655      100.0    185     2    US-08-486-596A-1       Sequence 1, Appli
  4       655      100.0    185     2    US-09-004-713-1        Sequence 1, Appli
  5       611       93.3    188     2    US-08-233-389C-3       Sequence 3, Appli
  6       611       93.3    188     2    US-08-801-863-3        Sequence 3, Appli
  7       611       93.3    188     2    US-08-486-596A-3       Sequence 3, Appli
  8       611       93.3    188     2    US-09-004-713-3        Sequence 3, Appli
  9       283       43.2     52     4    US-09-070-504-14       Sequence 14, Appl
 10       231       35.3     50     4    US-09-070-504-15       Sequence 15, Appl
 11       163       24.9     31     4    US-09-070-504-23       Sequence 23, Appl
 12       163       24.9     31     4    US-09-011-922A-3       Sequence 14, Appl
 13       163       24.9     31     4    US-09-011-922A-14      Sequence 14, Appl
 14       107       16.3      4     4    US-08-468-249A-20      Sequence 20, Appl
 15        75       11.5     20     4    US-08-011-922A-7       Sequence 7, Appli
 16        67.5     10.3     775     2   US-08-966-388-4        Sequence 4, Appli
 17        67.5     10.3     775     3   US-09-188-403-4        Sequence 4, Appli
 18        67.5     10.3     775     4   US-09-188-404-4        Sequence 4, Appli
 19        67.5     10.3     775     4   US-09-281-259-4        Sequence 4, Appli
 20        65.5     10.0     400     2   US-08-713-298B-2       Sequence 2, Appli
 21        65.5     10.0     400     2   US-08-870-180B-2       Sequence 2, Appli
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 25        65.5     10.0     462     2   US-08-870-180B-13      Sequence 13, Appl
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 28        65.5     10.0     467     4   US-08-945-574-1        Sequence 1, Appli
 29        65.5     10.0     754     2   US-08-941-262-1        Sequence 1, Appli
 30        65.5     10.0     755     2   US-08-941-262-3        Sequence 3, Appli
 31        65       9.9      485     1   US-08-453-956-15       Sequence 15, Appl
 32        65       9.9      485     1   US-08-086-631-15       Sequence 15, Appl
 33        65       9.9      485     1   US-08-452-930-15       Sequence 15, Appl
 34        65       9.9      2482    5   PCT-US93-08174-15      Sequence 15, Appl
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 36        64.5     9.8      491     1   US-08-328-254-6        Sequence 6, Appli
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 38        63.5     9.7      477     1   US-08-453-956-25       Sequence 25, Appl
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 45        61.5     9.4      454     3   US-09-189-627A-10      Sequence 10, Appl
                                         US-08-434-099A-27      Sequence 27, Appl
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ALIGNMENTS

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RESULT 1
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
;  APPLICANT: KITAMURA, Kazuo
;  APPLICANT: KANGAWA, Kenji
;  APPLICANT: MATSUO, Hisayuki
;  APPLICANT: ETO, Tanenao
;  TITLE OF INVENTION: ADRENOMEDULLIN
;  NUMBER OF SEQUENCES: 10
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: C/O FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/233,389C
;   FILING DATE: 26-APR-1994
;   CLASSIFICATION: 530
;  ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
;  INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 185 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-233-389C-1

  Query Match            100.0%;  Score 655;  DB 1;  Length 185;
  Best Local Similarity  100.0%;
  Matches  125;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy  121  SPQGY 125
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Db  142  SPQGY 146
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RESULT 2
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-1

Query Match   100.0%; Score 655; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-72;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  142  SPQGY 146
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RESULT 3
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-1

Query Match   100.0%; Score 655; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-72;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   82  DSSPDAARIRVKRYRYQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141

Qy  121  SPQGY 125
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Db  142  SPQGY 146
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RESULT 4
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-713-1

Query Match
Best Local Similarity 100.0%; Score 655; DB 2; Length 185;
Matches 125; Conservative 0; Pred. No. 1e-72; Mismatches 0; Indels 0; Gaps 0;

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Db 142 SPQGY 146
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RESULT 5
US-08-233-389C-3
Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-233-389C-3

Query Match
Best Local Similarity 91.2%; Score 611; DB 1; Length 188;
Matches 114; Conservative 8; Pred. No. 2.6e-67; Mismatches 3; Indels 0; Gaps 0;

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Qy 121 SPQGY 125
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Db 142 SPQGY 146
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RESULT 6
US-08-801-863-3
Sequence 3, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-801-863-3

Query Match
Best Local Similarity 93.3%; Score 611; DB 2; Length 188;
Matches 114; Conservative 8; Pred. No. 2.6e-67; Mismatches 3; Indels 0; Gaps 0;

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Db    142 SPQGY 146
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RESULT 7
US-08-486-596A-3
Sequence 3, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
   APPLICANT: KITAMURA, Kazuo
   APPLICANT: KANGAWA, Kenji
   APPLICANT: MATSUO, Hisayuki
   APPLICANT: ETO, Tanenao
   TITLE OF INVENTION: ADRENOMEDULLIN
   NUMBER OF SEQUENCES: 10
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: C/O FISH & NEAVE
   STREET: 1251 Avenue of the Americas
   CITY: New York
   STATE: NY
   COUNTRY: USA
   ZIP: 10020
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/486,596A
   FILING DATE: JUNE 7, 1995
   CLASSIFICATION: 530
   ATTORNEY/AGENT INFORMATION:
   NAME: HALEY Jr., James F.
   REGISTRATION NUMBER: 27,794
   REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
   TELECOMMUNICATION INFORMATION:
   TELEPHONE: (212) 596-9000
   TELEFAX: (212) 596-9090
   INFORMATION FOR SEQ ID NO: 3:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 188 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-486-596A-3

Query Match        93.3%;  Score 611;  DB 2;  Length 188;
Best Local Similarity  91.2%;  Pred. No. 2.6e-67;
Matches 114;  Conservative  8;  Mismatches  3;  Indels  0;  Gaps  0;

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Qy    121 SPQGY 125
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Db    142 SPQGY 146
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RESULT 8
US-09-004-713-3
Sequence 3, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
   APPLICANT: KITAMURA, Kazuo
   APPLICANT: KANGAWA, Kenji
   APPLICANT: MATSUO, Hisayuki
   APPLICANT: ETO, Tanenao
   TITLE OF INVENTION: ADRENOMEDULLIN
   NUMBER OF SEQUENCES: 10
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: C/O FISH & NEAVE
   STREET: 1251 Avenue of the Americas
   CITY: New York
   STATE: NY
   COUNTRY: USA
   ZIP: 10020
   COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/004,713
   FILING DATE: JANUARY 7, 1998
   CLASSIFICATION: 435
   ATTORNEY/AGENT INFORMATION:
   NAME: HALEY Jr., James F.
   REGISTRATION NUMBER: 27,794
   REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
   TELECOMMUNICATION INFORMATION:
   TELEPHONE: (212) 596-9000
   TELEFAX: (212) 596-9090
   INFORMATION FOR SEQ ID NO: 3:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 188 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
   MOLECULE TYPE: protein
US-09-004-713-3

Query Match        93.3%;  Score 611;  DB 2;  Length 188;
Best Local Similarity  91.2%;  Pred. No. 2.6e-67;
Matches 114;  Conservative  8;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
          |||||||:||||||||||||||||||:|||::|||:|||||||||:||:|||:||:||:
Db     22 ARLDVAAEFRKKWNKWALSRGKRELRSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81

Qy     61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141

Qy    121 SPQGY 125
          |||||
Db    142 SPQGY 146
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RESULT 9
US-09-070-504-14
Sequence 14, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
   APPLICANT: Smith, Derek D.
   APPLICANT: Saha, Shankar
   APPLICANT: Abel, Peter W.
   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
   NUMBER OF SEQUENCES: 23
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
   STREET: 119 No. 6268474th Fourth Street
   CITY: Minneapolis
   STATE: MN
```

(left fragment — continuation)

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;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/070,504
;     FILING DATE: 30-APR-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McCormack, Myra H
;     REGISTRATION NUMBER: 36,602
;     REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 612/305-1220
;     TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 50 amino acids
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RESULT 10

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US-09-070-504-14
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;     STREET: 119 No. 6268474th Fourth Street
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55401
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/070,504
;     FILING DATE: 30-APR-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McCormack, Myra H
;     REGISTRATION NUMBER: 36,602
;     REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 612/305-1220
;     TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 52 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide

  Query Match       43.2%;  Score 283;  DB 4;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-28;
  Matches  52;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   74  YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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RESULT 11

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US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;     STREET: 119 No. 6268474th Fourth Street
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55401
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/070,504
;     FILING DATE: 30-APR-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McCormack, Myra H
;     REGISTRATION NUMBER: 36,602
;     REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 612/305-1220
;     TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 31 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-09-070-504-23

  Query Match       35.3%;  Score 231;  DB 4;  Length 50;
  Best Local Similarity  84.6%;  Pred. No. 1.9e-21;
  Matches  44;  Conservative  3;  Mismatches  3;  Indels  2;  Gaps  1;

Qy   74  YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
         ||||||| || || |||||||||:|||||||||||||||||:|||||||||||
Db    1  YRQSMN--QGSRSTGCRFGTCTVQKLAHQIYQFTDKDGMAPRNKISPQGY 50
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RESULT 12

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US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
;   APPLICANT: Cuttitta, Frank; Martinez,

  Query Match       24.9%;  Score 163;  DB 4;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-13;
  Matches  31;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   95  TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
         |||||||||||||||||||||||||||||||
Db    1  TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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```
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
    STREET: 345 Park Avenue
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10154-0053
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy Disk
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: MS WORD 97
    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/011,922A
    FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/002,514
    FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/002,936
    FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/013,172
    FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/US96/13286
    FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
    NAME: Leslie A. Serunian
    REGISTRATION NUMBER: 35,353
    REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 758-4800
    TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
    LENGTH: 31 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
    NAME/KEY: P072
    OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Qy   95 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
        |||||||||||||||||||||||||||||||
Db    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Query Match     24.9%;   Score 163;  DB 4;  Length 31;
Best Local Similarity   100.0%;   Pred. No. 2.2e-13;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 13
US-09-011-922A-14
Sequence 14, Application US/09011922A
Patent No. 6320022
GENERAL INFORMATION:
    APPLICANT: Cuttitta, Frank; Martinez,
    APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
    APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
    APPLICANT: Karen; Macri, Charles
    TITLE OF INVENTION: Functional Role of
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TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
    STREET: 345 Park Avenue
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10154-0053
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy Disk
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: MS WORD 97
    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/011,922A
    FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/002,514
    FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/002,936
    FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/60/013,172
    FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/US96/13286
    FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
    NAME: Leslie A. Serunian
    REGISTRATION NUMBER: 35,353
    REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 758-4800
    TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
    LENGTH: 31 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
    OTHER INFORMATION: Synthetic homolog of
    OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Qy   95 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
        |||||||||||||||||||||||||||||||
Db    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Query Match     24.9%;   Score 163;  DB 4;  Length 31;
Best Local Similarity   100.0%;   Pred. No. 2.2e-13;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 14
US-09-011-922A-7
Sequence 7, Application US/09011922A
Patent No. 6320022
GENERAL INFORMATION:
    APPLICANT: Cuttitta, Frank; Martinez,
    APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
    APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
    APPLICANT: Karen; Macri, Charles
    TITLE OF INVENTION: Functional Role of
    TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
    TITLE OF INVENTION: Product (PAMP) in Human Pathology and
    TITLE OF INVENTION: Physiology
    NUMBER OF SEQUENCES: 17
```

CORRESPONDENCE ADDRESS:
  ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
  STREET: 345 Park Avenue
  CITY: New York
  STATE: NY
  COUNTRY: USA
  ZIP: 10154-0053
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy Disk
  COMPUTER: IBM PC Compatible
  OPERATING SYSTEM: MS WORD 97
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/011,922A
  FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,514
  FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,936
  FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/013,172
  FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US96/13286
  FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Leslie A. Serunian
  REGISTRATION NUMBER: 35,353
  REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 758-4800
  TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 20 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  HYPOTHETICAL: NO
  FRAGMENT TYPE: N-terminal
  FEATURE:
    NAME/KEY: PAMP-20
    OTHER INFORMATION: Proadrenomedullin N-
    OTHER INFORMATION: terminal 20 peptide
US-09-011-922A-7

Query Match   16.3%;   Score 107; DB 4; Length 20;
Best Local Similarity   100.0%; Pred. No. 9.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLDVASEFRKKWNKWALSR 20
      ||||||||||||||||||||
Db 1 ARLDVASEFRKKWNKWALSR 20

RESULT 15
US-08-468-249A-20
Sequence 20, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
  APPLICANT: Segre et al., Gino V.
  TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
  TITLE OF INVENTION: ENCODING SAME
  NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804

COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/468,249A
  FILING DATE: 06-JUN-1995
  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/864,475
  FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/681,702
  FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Fraser, Janis K.
  REGISTRATION NUMBER: 34,819
  REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 20:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 591 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-468-249A-20

Query Match   11.5%;   Score 75; DB 2; Length 591;
Best Local Similarity   32.5%; Pred. No. 0.72;
Matches 25; Conservative 12; Mismatches 26; Indels 14; Gaps 5;

Qy   4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-------TGLADV--KAG---PAQTLIRP 49
         :|:||||||||||||||: ||:| |||| |: || :||
Db 465 EVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP 524

Qy   50 QDMKGASRSPEDSSPDA 66
         ||:|:| | | |
Db 525 ATTNGHSQLPGHAKPGA 541

Search completed: October 17, 2002, 15:22:03
Job time : 8.55049 secs

OM protein - protein search, using sw model

GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

Run on: October 17, 2002, 15:20:12 ; Search time 12.4495 Seconds
(without alignments)
357.079 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence: 1 VSVALMYLGSLAFLGADTAR.........SKPQAHGAPAPPSGSAPHFL 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	947	100.0	185	1	US-08-233-389C-1	Sequence 1, Appli
2	947	100.0	185	1	US-08-801-863-1	Sequence 1, Appli
3	947	100.0	185	2	US-08-801-863-1	Sequence 1, Appli
4	947	100.0	185	2	US-09-004-713-1	Sequence 1, Appli
5	817	86.3	188	2	US-08-233-389C-3	Sequence 3, Appli
6	817	86.3	188	2	US-08-801-863-3	Sequence 3, Appli
7	817	86.3	188	2	US-08-486-596A-3	Sequence 3, Appli
8	817	86.3	188	2	US-09-004-713-3	Sequence 3, Appli
9	283	29.9	52	4	US-09-070-504-14	Sequence 14, Appl
10	231	24.4	50	4	US-09-070-504-15	Sequence 15, Appl
11	163	17.2	31	4	US-09-070-504-23	Sequence 23, Appl
12	163	17.2	31	4	US-09-011-922A-3	Sequence 3, Appl
13	163	17.2	31	4	US-09-011-922A-14	Sequence 14, Appl
14	107	11.3	20	4	US-09-011-922A-7	Sequence 7, Appli
15	86.5	9.1	401	4	US-09-390-721-2	Sequence 2, Appli
16	80	8.4	496	2	US-08-949-637-2	Sequence 2, Appli
17	80	8.4	496	4	US-09-291-488-2	Sequence 2, Appli
18	79	8.3	450	1	US-08-444-734A-8	Sequence 8, Appli
19	78	8.2	450	1	US-08-194-338-5	Sequence 5, Appli
20	76.5	8.1	490	1	US-08-472-028A-10	Sequence 10, Appli
21	76.5	8.1	490	4	US-09-071-296-10	Sequence 10, Appli
22	76.5	8.1	490	4	US-09-196-268-10	Sequence 10, Appli
23	76.5	8.1	490	4	US-09-015-683-10	Sequence 10, Appli
24	76.5	8.1	490	4	US-09-191-598-10	Sequence 10, Appli
25	76	8.0	373	4	US-09-039-198A-14	Sequence 14, Appl
26	76	8.0	373	4	US-09-039-198A-15	Sequence 15, Appl
27	76	8.0	387	2	US-08-486-839-6	Sequence 6, Appli
28	76	8.0	387	3	US-09-151-011-6	Sequence 6, Appli
29	76	8.0	387	4	US-09-343-623-6	Sequence 6, Appli
30	76	8.0	410	1	US-07-945-283-4	Sequence 4, Appli
31	76	8.0	466	3	US-08-486-839-4	Sequence 4, Appli
32	76	8.0	466	3	US-09-151-011-4	Sequence 4, Appli
33	76	8.0	466	4	US-09-039-198A-2	Sequence 2, Appli
34	76	8.0	466	4	US-09-039-198A-4	Sequence 4, Appli
35	75	7.9	466	2	US-09-343-623-4	Sequence 4, Appli
36	74.5	7.9	591	2	US-08-468-249A-20	Sequence 20, Appl
37	74.5	7.9	933	4	US-08-764-870-14	Sequence 14, Appl
38	74.5	7.9	933	4	US-08-980-115-14	Sequence 14, Appl
39	74	7.8	302	2	US-08-893-853-3	Sequence 3, Appli
40	74	7.8	302	3	US-09-113-921-3	Sequence 3, Appli
41	73.5	7.8	1323	1	US-08-026-13BE-4	Sequence 4, Appli
42	72	7.6	434	3	US-08-337-602-2	Sequence 2, Appli
43	72	7.6	434	4	US-08-558-135-2	Sequence 2, Appli
44	72	7.6	2336	4	US-09-268-163-10	Sequence 10, Appl
45	70	7.4	423	4	US-08-939-366-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-389C-1

Query Match 100.0%; Score 947; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

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Qy   61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy  181  FL 182
         ||
Db  184  FL 185
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RESULT 2
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/801,863
;   FILING DATE: CONCURRENTLY HEREWITH
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-801-863-1

Query Match   100.0%; Score 947; DB 2; Length 185;
Best Local Similarity   100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  63

Qy   61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy  181  FL 182
         ||
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Db  184  FL 185
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RESULT 3
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/486,596A
;   FILING DATE: JUNE 7, 1995
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-486-596A-1

Query Match   100.0%; Score 947; DB 2; Length 185;
Best Local Similarity   100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  63

Qy   61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy  181  FL 182
         ||
Db  184  FL 185
```

RESULT 4
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji

```
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
    ADDRESSEE: c/o FISH & NEAVE
    STREET: 1251 Avenue of the Americas
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10020
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/004,713
    FILING DATE: JANUARY 7, 1998
    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    NAME: HALEY Jr., James F.
    REGISTRATION NUMBER: 27,794
    REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 596-9000
    TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 185 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein
US-09-004-713-1

Query Match           100.0%;   Score 947;  DB 2;   Length 185;
Best Local Similarity 100.0%;   Pred. No. 4.9e-99;
Matches 182;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy  181 FL 182
          ||
Db  184 FL 185

RESULT 5
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
    APPLICANT: KITAMURA, Kazuo
    APPLICANT: KANGAWA, Kenji
    APPLICANT: MATSUO, Hisayuki
    APPLICANT: ETO, Tanenao
    TITLE OF INVENTION: ADRENOMEDULLIN
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: c/o FISH & NEAVE
        STREET: 1251 Avenue of the Americas
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10020
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/233,389C
        FILING DATE: 26-APR-1994
        CLASSIFICATION: 530
    ATTORNEY/AGENT INFORMATION:
        NAME: HALEY Jr., James F.
        REGISTRATION NUMBER: 27,794
        REFERENCE/DOCKET NUMBER: SHGN-5
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 596-9000
        TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 188 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-233-389C-3

Query Match           86.3%;   Score 817;  DB 1;   Length 188;
Best Local Similarity 89.1%;   Pred. No. 2.2e-84;
Matches 156;  Conservative 10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
          | ||||||||||||||||||||||||||||||||||||||||||::||:|||::||||
Db    4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
          ||:||||||::||:|||| :|:|||| | |||||||||||||||||||||||||||||||
Db   64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
          ||||||| |||| ||||||||||||||||||| |:| :|||||| :
Db  124 IYQFTDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178

RESULT 6
US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
    APPLICANT: KITAMURA, Kazuo
    APPLICANT: KANGAWA, Kenji
    APPLICANT: MATSUO, Hisayuki
    APPLICANT: ETO, Tanenao
    TITLE OF INVENTION: ADRENOMEDULLIN
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: c/o FISH & NEAVE
        STREET: 1251 Avenue of the Americas
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10020
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/801,863
        FILING DATE: CONCURRENTLY HEREWITH
        CLASSIFICATION: 530
    ATTORNEY/AGENT INFORMATION:
        NAME: HALEY Jr., James F.
        REGISTRATION NUMBER: 27,794
        REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-3

Query Match   86.3%;   Score 817; DB 2; Length 188;
Best Local Similarity 89.1%;   Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```
Qy    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  60
          ||||||||||||||||||||||||| ||||||||||||||||| ||||| ||| |||| 
Db    4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP  63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
          ||| ||||| | ||| : |||||||||||||||||||||||||||||||||||||||||
Db   64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
          ||||||| ||| ||||||||||||||||||||  |||| ||||||||||| |
Db  124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178
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RESULT 7
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-3

Query Match   86.3%;   Score 817; DB 2; Length 188;
Best Local Similarity 89.1%;   Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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Qy    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  60
          ||||||||||||||||||||||||| ||||||||||||||||| ||||| ||| |||| 
Db    4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP  63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
          ||| ||||| | ||| : |||||||||||||||||||||||||||||||||||||||||
Db   64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
          ||||||| ||| ||||||||||||||||||||  |||| ||||||||||| |
Db  124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178
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RESULT 8
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-3

Query Match   86.3%;   Score 817; DB 2; Length 188;
Best Local Similarity 89.1%;   Pred. No. 2.2e-84;   Indels 0; Gaps 0;
Matches 156; Conservative 10; Mismatches 9;

```
Qy    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP  60
          ||||||||||||||||||||||||| ||||||||||||||||| ||||| ||| |||| 
Db    4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP  63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
          ||| ||||| | ||| : |||||||||||||||||||||||||||||||||||||||||
Db   64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
          ||||||| ||| ||||||||||||||||||||  |||| ||||||||||| |
Db  124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178
```

RESULT 9
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;   STREET: 119 No. 6268474th Fourth Street
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,504
;   FILING DATE: 30-APR-1998
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McCormack, Myra H
;   REGISTRATION NUMBER: 36,602
;   REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612/305-1220
;   TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 52 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-070-504-14

Query Match   29.9%; Score 283; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.6e-25;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;   STREET: 119 No. 6268474th Fourth Street
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,504
;   FILING DATE: 30-APR-1998
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McCormack, Myra H
;   REGISTRATION NUMBER: 36,602
;   REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612/305-1220
;   TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 50 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-070-504-15

Query Match   24.4%; Score 231; DB 4; Length 50;
Best Local Similarity 84.6%; Pred. No. 3.8e-19;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Qy 92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
        |||||| |||| ::||||||||||| :||:|||||||| :|||:|||||||
Db   1 YRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 50

RESULT 11
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;   STREET: 119 No. 6268474th Fourth Street
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,504
;   FILING DATE: 30-APR-1998
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McCormack, Myra H
;   REGISTRATION NUMBER: 36,602
;   REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612/305-1220
;   TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 31 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-070-504-23

Query Match   17.2%;   Score 163;   DB 4;   Length 31;
Best Local Similarity 100.0%;   Pred. No. 9.2e-12;
Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
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Db   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 12
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
;   APPLICANT: Cuttitta, Frank; Martinez,
;   APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
;   APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
;   APPLICANT: Karen; Macri, Charles
;   TITLE OF INVENTION: Functional Role of
;   TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
;   TITLE OF INVENTION: Product (PAMP) in Human Pathology and
;   TITLE OF INVENTION: Physiology
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;   STREET: 345 Park Avenue
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10154-0053
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: MS WORD 97
;   SOFTWARE: ASCII
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/011,922A
;   FILING DATE: 17-Feb-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/002,514
;   FILING DATE: 18-Aug-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/002,936
;   FILING DATE: 30-Aug-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/013,172
;   FILING DATE: 12-Mar-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/13286
;   FILING DATE: 16-Aug-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Leslie A. Serunian
;   REGISTRATION NUMBER: 35,353
;   REFERENCE/DOCKET NUMBER: 2026-4202US3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 758-4800
;   TELEFAX: (212) 751-6849
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 31 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   FEATURE:
;   NAME/KEY: P072
;   OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Query Match   17.2%;   Score 163;   DB 4;   Length 31;
Best Local Similarity 100.0%;   Pred. No. 9.2e-12;
Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 13
US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
;   APPLICANT: Cuttitta, Frank; Martinez,
;   APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
;   APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
;   APPLICANT: Karen; Macri, Charles
;   TITLE OF INVENTION: Functional Role of
;   TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
;   TITLE OF INVENTION: Product (PAMP) in Human Pathology and
;   TITLE OF INVENTION: Physiology
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;   STREET: 345 Park Avenue
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10154-0053
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: MS WORD 97
;   SOFTWARE: ASCII
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/011,922A
;   FILING DATE: 17-Feb-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/002,514
;   FILING DATE: 18-Aug-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/002,936
;   FILING DATE: 30-Aug-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/60/013,172
;   FILING DATE: 12-Mar-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/13286
;   FILING DATE: 16-Aug-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Leslie A. Serunian
;   REGISTRATION NUMBER: 35,353
;   REFERENCE/DOCKET NUMBER: 2026-4202US3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 758-4800
;   TELEFAX: (212) 751-6849
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 31 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   FEATURE:
;   OTHER INFORMATION: Synthetic homolog of
;   OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Query Match   17.2%;   Score 163;   DB 4;   Length 31;
Best Local Similarity 100.0%;   Pred. No. 9.2e-12;
Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
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Db   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 14
US-09-011-922A-7
; Sequence 7, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: PAMP-20
; OTHER INFORMATION: Proadrenomedullin N-
; OTHER INFORMATION: terminal 20 peptide
US-09-011-922A-7

Query Match   11.3%; Score 107; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 20; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 19 ARLDVASEFRKKWNKWALSR 38
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Db   1 ARLDVASEFRKKWNKWALSR 20

RESULT 15
US-09-390-721-2
; Sequence 2, Application US/09390721
; Patent No. 6197591
; GENERAL INFORMATION:
; APPLICANT: STUTZMAN-ENGWALL, KIM J.
; APPLICANT: PRICE, BRENDA S.
; TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED
; TITLE OF INVENTION: AVERMECTIN PRODUCTION
; FILE REFERENCE: PC9944A
; CURRENT APPLICATION NUMBER: US/09/390,721
; CURRENT FILING DATE: 1999-09-07
; EARLIER APPLICATION NUMBER: 60/100,134
; EARLIER FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-09-390-721-2

Query Match   9.1%; Score 86.5; DB 4; Length 401;
Best Local Similarity 20.5%; Pred. No. 0.12;
Matches 52; Conservative 26; Mismatches 83; Indels 93; Gaps   8;

Qy   2 SVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSS-------------- 47
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Db 157 SPGLLLLGFAALLGA----------------WQLGRAARQRRAFAVRAAEQLAQRAVTE 199

Qy 48 --------SYPTGLADVKAGPAQTL--IRPQDMKGASRSPEDSSPDAARIRVKRY 92
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Db 200 ERLRIARELHDVTHSMGLIAVKVGVANHVLHIRPQEAYDALQVIERTSRTALN-DMRRM 258

Qy 93 RQSMNNFQGLR---SFGCRFGTCTVQKLAHQ--------------------IYQFTDKDK 129
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Db 259 LGVLRTSEGERQSAALGPLPGALALPDLVGQAGAQLTMRGVESLPDGVALAVYRIVQEAL 318

Qy 130 DNVA------PRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHG-------------- 169
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Db 319 TNVAKHAGPEARCRVAVDANGHGVRLEITDDGGDRSPLAPKPGGHGIVGMRERVALYGGT 378

Qy 170 ---APAPPSGSAPH 180
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Db 379 FAAGPRPEGGFAVH 392

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Job time : 13.4495 secs

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                GenCore version 5.1.3
        Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      October 17, 2002, 14:45:20 ; Search time 4.53865 Seconds
                                           (without alignments)
                                         279.848 Million cell updates/sec

Title:           US-10-018-924-2_COPY_95_146
Perfect score:   283
Sequence:        1 YRQSMNNFQGLRSFGCRFGT..........FTDKDKDNVAPRSKISPQGY 52

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:   231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued_Patents_AA:*
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   2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	283	100.0	52	4	US-09-070-504-14	Sequence 14, Appl
2	283	100.0	185	2	US-08-233-389C-1	Sequence 1, Appli
3	283	100.0	185	2	US-08-801-863-1	Sequence 1, Appli
4	283	100.0	185	2	US-09-004-713-1	Sequence 1, Appli
5	283	100.0	188	1	US-08-233-389C-3	Sequence 3, Appli
6	277	97.9	188	1	US-08-801-863-3	Sequence 3, Appli
7	277	97.9	188	2	US-08-486-596A-3	Sequence 3, Appli
8	277	97.9	188	2	US-08-486-596A-3	Sequence 3, Appli
9	277	97.9	50	4	US-09-004-713-3	Sequence 3, Appli
10	231	81.6	31	4	US-09-070-504-15	Sequence 15, Appl
11	163	57.6	31	4	US-09-070-504-23	Sequence 23, Appli
12	163	57.6	13	4	US-09-011-922A-3	Sequence 3, Appli
13	163	57.6	858	4	US-09-011-922A-14	Sequence 14, Appl
14	57	20.1	508	1	US-09-011-922A-2	Sequence 2, Appli
15	56	19.8	529	1	US-08-265-628-2	Sequence 10, Appl
16	53	18.7	529	2	US-07-891-942G-10	Sequence 8, Appli
17	53	18.7	529	2	US-07-891-942G-9	Sequence 19, Appl
18	53	18.7	537	2	US-08-370-909-19	Sequence 8, Appli
19	53	18.7	560	4	US-08-504-048-8	Sequence 12, Appl
20	53	18.7	775	2	US-08-540-022D-12	Sequence 5, Appli
21	52	18.4	775	2	US-07-891-942G-5	Sequence 4, Appli
22	52	18.4	775	3	US-08-966-388-4	Sequence 4, Appli
23	52	18.4	775	4	US-09-188-404-4	Sequence 4, Appli
24	52	18.4	775	4	US-09-188-404-4	Sequence 4, Appli
25	51	18.0	775	2	US-09-281-259-4	Sequence 4, Appli
26	51	18.0	10	2	US-08-934-222-17	Sequence 17, Appl
27	51	18.0	10	2	US-08-933-402-17	Sequence 17, Appl
28	51	18.0	10	2	US-09-207-621-17	Sequence 17, Appl
29	51	18.0	10	2	US-08-532-818-17	Sequence 17, Appl
30	51	18.0	10	3	US-09-231-797-17	Sequence 17, Appl
31	51	18.0	10	3	US-08-934-224-17	Sequence 17, Appl
32	51	18.0	10	3	US-08-933-843-17	Sequence 17, Appl
33	51	18.0	10	4	US-08-934-223-17	Sequence 17, Appl
34	51	18.0	10	4	US-09-413-492-17	Sequence 17, Appl
35	50	17.8	1261	4	US-09-439-313-538	Sequence 538, App
36	50	17.7	364	1	US-08-318-831-6	Sequence 6, Appli
37	50	17.7	423	2	US-08-290-731C-10	Sequence 10, Appl
38	50	17.7	1319	2	US-09-356-952-2	Sequence 2, Appli
39	50	17.7	1336	3	US-08-290-731C-6	Sequence 6, Appli
40	49	17.3	630	3	US-08-797-366-3	Sequence 3, Appli
41	49	17.3	630	3	US-08-956-268-3	Sequence 3, Appli
42	49	17.3	138	1	US-08-470-179-29	Sequence 29, Appl
43	48	17.0	795	3	US-09-031-563-23	Sequence 23, Appl
44	47.5	16.8	430	2	US-08-290-731C-9	Sequence 9, Appli
45	47	16.6				

ALIGNMENTS

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RESULT 1
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;   STREET: 119 No. 6268474th Fourth Street
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55401
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,504
;   FILING DATE: 30-APR-1998
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McCormack, Myra H
;   REGISTRATION NUMBER: 36,602
;   REFERENCE/DOCKET NUMBER: 180.00020101
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612/305-1220
;   TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 52 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide,
US-09-070-504-14

  Query Match            100.0%;  Score 283;  DB 4;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 8e-35;
  Matches   52;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 2
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/233,389C
;   FILING DATE: 26-APR-1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-233-389C-1

Query Match   100.0%; Score 283; DB 1; Length 185;
Best Local Similarity   100.0%; Pred. No. 3.8e-34;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 3
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/801,863
;   FILING DATE: CONCURRENTLY HEREWITH
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-801-863-1

Query Match   100.0%; Score 283; DB 2; Length 185;
Best Local Similarity   100.0%; Pred. No. 3.8e-34;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 4
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/486,596A
;   FILING DATE: JUNE 7, 1995
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-486-596A-1

Query Match   100.0%;   Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 5
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/004,713
;   FILING DATE: JANUARY 7, 1998
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-004-713-1

Query Match   100.0%;   Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 6
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE

;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/233,389C
;   FILING DATE: 26-APR-1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 188 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-233-389C-3

Query Match   97.9%;   Score 277; DB 1; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-33;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        ||||||||||||||||||||||||||||||||||||||| |||||||||||
Db 95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 7
US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/801,863
;   FILING DATE: CONCURRENTLY HEREWITH
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:

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;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  188 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-801-863-3

Query Match             97.9%;  Score 277;  DB 2;  Length 188;
Best Local Similarity   98.1%;  Pred. No. 3e-33;
  Matches   51;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 8
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
;   GENERAL INFORMATION:
;     APPLICANT:  KITAMURA, Kazuo
;     APPLICANT:  KANGAWA, Kenji
;     APPLICANT:  MATSUO, Hisayuki
;     APPLICANT:  ETO, Tanenao
;     TITLE OF INVENTION:  ADRENOMEDULLIN
;     NUMBER OF SEQUENCES:  10
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  c/o FISH & NEAVE
;       STREET:  1251 Avenue of the Americas
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10020
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/486,596A
;       FILING DATE:  JUNE 7, 1995
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HALEY Jr., James F.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  SHGN-5 DIV1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  188 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-486-596A-3

Query Match             97.9%;  Score 277;  DB 2;  Length 188;
Best Local Similarity   98.1%;  Pred. No. 3e-33;
  Matches   51;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 9
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
;   GENERAL INFORMATION:
;     APPLICANT:  KITAMURA, Kazuo
```

```
;     APPLICANT:  KANGAWA, Kenji
;     APPLICANT:  MATSUO, Hisayuki
;     APPLICANT:  ETO, Tanenao
;     TITLE OF INVENTION:  ADRENOMEDULLIN
;     NUMBER OF SEQUENCES:  10
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  c/o FISH & NEAVE
;       STREET:  1251 Avenue of the Americas
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10020
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/004,713
;       FILING DATE:  JANUARY 7, 1998
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HALEY Jr., James F.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  SHGN-5 DIV2 CON
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  188 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-004-713-3

Query Match             97.9%;  Score 277;  DB 2;  Length 188;
Best Local Similarity   98.1%;  Pred. No. 3e-33;
  Matches   51;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
;   GENERAL INFORMATION:
;     APPLICANT:  Smith, Derek D.
;     APPLICANT:  Saha, Shankar
;     APPLICANT:  Abel, Peter W.
;     TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;     TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;       STREET:  119 No. 6268474th Fourth Street
;       CITY:  Minneapolis
;       STATE:  MN
;       COUNTRY:  USA
;       ZIP:  55401
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/070,504
;       FILING DATE:  30-APR-1998
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
```

```
         NAME: McCormack, Myra H
         REGISTRATION NUMBER: 36,602
         REFERENCE/DOCKET NUMBER: 180.00020101
      TELECOMMUNICATION INFORMATION:
         TELEPHONE: 612/305-1220
         TELEFAX: 612/305-1228
   INFORMATION FOR SEQ ID NO: 15:
      SEQUENCE CHARACTERISTICS:
         LENGTH: 50 amino acids
         TYPE: amino acid
         STRANDEDNESS: single
         TOPOLOGY: linear
      MOLECULE TYPE: peptide
US-09-070-504-15

Query Match      81.6%;  Score 231;  DB 4;  Length 50;
Best Local Similarity  84.6%;  Pred. No. 3.6e-27;
Matches   44;  Conservative   3;  Mismatches   3;  Indels   2;  Gaps   1;

Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
          ||||||  |||| ||||||||| ::||||||||||||||| :|||:||||||
Db    1 YRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 50

RESULT 11
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
      APPLICANT: Smith, Derek D.
      APPLICANT: Saha, Shankar
      APPLICANT: Abel, Peter W.
      TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
      TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
      NUMBER OF SEQUENCES: 23
      CORRESPONDENCE ADDRESS:
         ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
         STREET: 119 No. 6268474th Fourth Street
         CITY: Minneapolis
         STATE: MN
         COUNTRY: USA
         ZIP: 55401
      COMPUTER READABLE FORM:
         MEDIUM TYPE: Floppy disk
         COMPUTER: IBM PC compatible
         OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/070,504
         FILING DATE: 30-APR-1998
         CLASSIFICATION:
      ATTORNEY/AGENT INFORMATION:
         NAME: McCormack, Myra H
         REGISTRATION NUMBER: 36,602
         REFERENCE/DOCKET NUMBER: 180.00020101
      TELECOMMUNICATION INFORMATION:
         TELEPHONE: 612/305-1220
         TELEFAX: 612/305-1228
   INFORMATION FOR SEQ ID NO: 23:
      SEQUENCE CHARACTERISTICS:
         LENGTH: 31 amino acids
         TYPE: amino acid
         STRANDEDNESS: single
         TOPOLOGY: linear
      MOLECULE TYPE: peptide
US-09-070-504-23

Query Match      57.6%;  Score 163;  DB 4;  Length 31;
Best Local Similarity  100.0%;  Pred. No. 2.2e-17;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
         |||||||||||||||||||||||||||||||
Db    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 12
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
      APPLICANT: Cuttitta, Frank; Martinez,
      APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
      APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
      APPLICANT: Karen; Macri, Charles
      TITLE OF INVENTION: Functional Role of
      TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
      TITLE OF INVENTION: Product (PAMP) in Human Pathology and
      TITLE OF INVENTION: Physiology
      NUMBER OF SEQUENCES: 17
      CORRESPONDENCE ADDRESS:
         ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
         STREET: 345 Park Avenue
         CITY: New York
         STATE: NY
         COUNTRY: USA
         ZIP: 10154-0053
      COMPUTER READABLE FORM:
         MEDIUM TYPE: Floppy Disk
         COMPUTER: IBM PC Compatible
         OPERATING SYSTEM: MS WORD 97
         SOFTWARE: ASCII
      CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/011,922A
         FILING DATE: 17-Feb-1998
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: US/60/002,514
         FILING DATE: 18-Aug-1995
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: US/60/002,936
         FILING DATE: 30-Aug-1995
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: US/60/013,172
         FILING DATE: 12-Mar-1996
      PRIOR APPLICATION DATA:
         APPLICATION NUMBER: PCT/US96/13286
         FILING DATE: 16-Aug-1996
      ATTORNEY/AGENT INFORMATION:
         NAME: Leslie A. Serunian
         REGISTRATION NUMBER: 35,353
         REFERENCE/DOCKET NUMBER: 2026-4202US3
      TELECOMMUNICATION INFORMATION:
         TELEPHONE: (212) 758-4800
         TELEFAX: (212) 751-6849
   INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
         LENGTH: 31 amino acids
         TYPE: amino acid
         TOPOLOGY: linear
      MOLECULE TYPE: peptide
      HYPOTHETICAL: NO
      FEATURE:
         NAME/KEY: P072
         OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Query Match      57.6%;  Score 163;  DB 4;  Length 31;
Best Local Similarity  100.0%;  Pred. No. 2.2e-17;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
         |||||||||||||||||||||||||||||||
Db    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 13
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US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
    APPLICANT: Cuttitta, Frank; Martinez,
    APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
    APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
    APPLICANT: Karen; Macri, Charles
    TITLE OF INVENTION: Functional Role of
    TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
    TITLE OF INVENTION: Product (PAMP) in Human Pathology and
    TITLE OF INVENTION: Physiology
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
        STREET: 345 Park Avenue
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10154-0053
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy Disk
        COMPUTER: IBM PC Compatible
        OPERATING SYSTEM: MS WORD 97
        SOFTWARE: ASCII
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/011,922A
        FILING DATE: 17-Feb-1998
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/002,514
        FILING DATE: 18-Aug-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/002,936
        FILING DATE: 30-Aug-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/013,172
        FILING DATE: 12-Mar-1996
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/US96/13286
        FILING DATE: 16-Aug-1996
    ATTORNEY/AGENT INFORMATION:
        NAME: Leslie A. Serunian
        REGISTRATION NUMBER: 35,353
        REFERENCE/DOCKET NUMBER: 2026-4202US3
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 758-4800
        TELEFAX: (212) 751-6849
    INFORMATION FOR SEQ ID NO: 14:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 31 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
        MOLECULE TYPE: peptide
        HYPOTHETICAL: NO
        FEATURE:
        OTHER INFORMATION: Synthetic homolog of
        OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Query Match   57.6%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        |||||||||||||||||||||||||||||||
Db   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 14
US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
    APPLICANT: Cuttitta, Frank; Martinez,
    APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
    APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
    APPLICANT: Karen; Macri, Charles
    TITLE OF INVENTION: Functional Role of
    TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
    TITLE OF INVENTION: Product (PAMP) in Human Pathology and
    TITLE OF INVENTION: Physiology
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
        STREET: 345 Park Avenue
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10154-0053
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy Disk
        COMPUTER: IBM PC Compatible
        OPERATING SYSTEM: MS WORD 97
        SOFTWARE: ASCII
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/011,922A
        FILING DATE: 17-Feb-1998
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/002,514
        FILING DATE: 18-Aug-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/002,936
        FILING DATE: 30-Aug-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/60/013,172
        FILING DATE: 12-Mar-1996
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/US96/13286
        FILING DATE: 16-Aug-1996
    ATTORNEY/AGENT INFORMATION:
        NAME: Leslie A. Serunian
        REGISTRATION NUMBER: 35,353
        REFERENCE/DOCKET NUMBER: 2026-4202US3
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 758-4800
        TELEFAX: (212) 751-6849
    INFORMATION FOR SEQ ID NO: 2:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 13 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
        MOLECULE TYPE: peptide
        HYPOTHETICAL: NO
        FEATURE:
        NAME/KEY: P071
        OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2

Query Match   20.1%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 HQIYQFTDKD 37
        ||||||||||
Db   4 HQIYQFTDKD 13

RESULT 15
US-08-265-628-2
; Sequence 2, Application US/08265628
; Patent No. 5821094
; GENERAL INFORMATION:
    APPLICANT: Rothstein, Steven J.
    APPLICANT: Goring, Daphne
    TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
    TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE

```
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
    ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
    STREET:  500 W. Madison St.   Suite 3400
    CITY:  Chicago
    STATE:  Illinois
    COUNTRY:  USA
    ZIP:. 60661
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/265,628
    FILING DATE:
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US/07/959,945
    FILING DATE:
    APPLICATION NUMBER:  US 07/847,564
    FILING DATE:  03-MAR-1992
ATTORNEY/AGENT INFORMATION:
    NAME:  Pochopien Ph.D., Donald J.
    REGISTRATION NUMBER:  32,167
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  312-707-8889
    TELEFAX:  312-707-9155
INFORMATION FOR SEQ ID NO:  2:
SEQUENCE CHARACTERISTICS:
    LENGTH:  858 amino acids
    TYPE:  amino acid
    TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-08-265-628-2
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Query Match         19.8%;   Score 56;   DB 2;   Length 858;
Best Local Similarity   39.5%;   Pred. No. 8;
Matches   15;   Conservative   6;   Mismatches   13;   Indels   4;   Gaps   2;

Qy    6  NNFQGLRS---FGCRF-GTCTVQKLAHQIYQFTDKDKD 39
            |  :| | |    | | |    |||:: :| ||||  :: ||||
Db  218  NGVRGYRSGPWNGVRFNGIPEDQKLSYMYYNFTDNSEE 255
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Search completed: October 17, 2002, 14:48:43
Job time : 5.53865 secs

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                    GenCore version 5.1.3
            Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 17, 2002, 14:45:20 ; Search time 3.49127 Seconds
                                        (without alignments)
                                       279.848 Million cell updates/sec

Title:           US-10-018-924-2_COPY_107_146
Perfect score:   219
Sequence:        1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:      231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	219	100.0	52	4	US-09-070-504-14	Sequence 14, Appl
2	219	100.0	185	1	US-08-233-389C-1	Sequence 1, Appli
3	219	100.0	185	2	US-08-801-863-1	Sequence 1, Appli
4	219	100.0	185	2	US-08-486-596A-1	Sequence 1, Appli
5	219	100.0	185	1	US-09-004-713-1	Sequence 1, Appli
6	213	97.3	188	1	US-08-233-389C-3	Sequence 3, Appli
7	213	97.3	188	2	US-08-801-863-3	Sequence 3, Appli
8	213	97.3	188	2	US-08-486-596A-3	Sequence 3, Appli
9	213	97.3	188	2	US-09-004-713-3	Sequence 3, Appli
10	196	89.5	50	4	US-09-070-504-15	Sequence 15, Appl
11	163	74.4	31	4	US-09-070-504-23	Sequence 23, Appl
12	163	74.4	31	4	US-09-011-922A-3	Sequence 3, Appli
13	163	74.4	31	4	US-09-011-922A-14	Sequence 14, Appl
14	57	26.0	13	4	US-09-011-922A-2	Sequence 2, Appli
15	52	23.7	775	3	US-08-966-388-4	Sequence 4, Appli
16	52	23.7	775	4	US-09-188-403-4	Sequence 4, Appli
17	52	23.7	775	4	US-09-188-404-4	Sequence 4, Appli
18	52	23.7	775	4	US-09-281-259-4	Sequence 4, Appli
19	51	23.3	10	2	US-08-934-222-17	Sequence 17, Appl
20	51	23.3	10	2	US-08-933-402-17	Sequence 17, Appl
21	51	23.3	10	2	US-09-207-621-17	Sequence 17, Appl
22	51	23.3	10	2	US-08-532-818-17	Sequence 17, Appl
23	51	23.3	10	3	US-08-231-797-17	Sequence 17, Appl
24	51	23.3	10	3	US-08-934-224-17	Sequence 17, Appl
25	51	23.3	10	3	US-08-933-843-17	Sequence 17, Appl
26	51	23.3	10	4	US-08-934-223-17	Sequence 17, Appl
27	51	23.3	10	4	US-09-413-492-17	Sequence 17, Appl
28	51	23.3	1261	4	US-09-439-313-538	Sequence 538, App
29	50.5	23.1	858	2	US-08-265-628-2	Sequence 2, Appli
30	47	21.5	1477	3	US-08-492-459-10	Sequence 10, Appl
31	47	21.5	1477	3	US-08-423-752-10	Sequence 10, Appl
32	47	21.5	1477	3	US-08-945-994-3	Sequence 3, Appli
33	47	21.5	1477	4	US-08-716-873-24	Sequence 24, Appl
34	47	21.5	1477	4	US-09-368-431-24	Sequence 24, Appl
35	47	21.5	1477	4	US-09-411-006-10	Sequence 10, Appl
36	46.5	21.0	131	4	US-09-247-155-174	Sequence 174, App
37	46	21.0	42	4	US-09-167-681-47	Sequence 47, Appl
38	46	21.0	336	4	US-09-141-206-7	Sequence 7, Appli
39	46	21.0	922	4	US-09-141-206-6	Sequence 6, Appli
40	46	21.0	933	4	US-09-141-206-2	Sequence 2, Appli
41	46	21.0	933	4	US-09-107-149-2	Sequence 2, Appli
42	46	21.0	933	4	US-09-107-149-17	Sequence 17, Appl
43	46	21.0	1622	4	US-08-972-927-6	Sequence 6, Appli
44	45	20.5	932	3	US-08-968-752B-6	Sequence 6, Appli
45	44.5	20.3	148	1	US-08-207-904-15	Sequence 15, Appl

ALIGNMENTS

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RESULT 1
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;  APPLICANT:  Smith, Derek D.
;  APPLICANT:  Saha, Shankar
;  APPLICANT:  Abel, Peter W.
;  TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;  TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;  NUMBER OF SEQUENCES:  23
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;    STREET:  119 No. 6268474th Fourth Street
;    CITY:  Minneapolis
;    STATE:  MN
;    COUNTRY:  USA
;    ZIP:  55401
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/09/070,504
;    FILING DATE:  30-APR-1998
;    CLASSIFICATION:
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  McCormack, Myra H
;    REGISTRATION NUMBER:  36,602
;    REFERENCE/DOCKET NUMBER:  180.00020101
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  612/305-1220
;    TELEFAX:  612/305-1228
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  52 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;  MOLECULE TYPE:  peptide
US-09-070-504-14

Query Match             100.0%;  Score 219; DB 4;  Length 52;
Best Local Similarity   100.0%;           Pred. No. 3.6e-26;
Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||||||||||||||||||||||||
Db   13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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RESULT 2
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/233,389C
;   FILING DATE: 26-APR-1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-233-389C-1

Query Match   100.0%; Score 219; DB 1; Length 185;
Best Local Similarity   100.0%; Pred. No. 1.6e-25;
Matches   40; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 3
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/801,863
;   FILING DATE: CONCURRENTLY HEREWITH
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-801-863-1

Query Match   100.0%; Score 219; DB 2; Length 185;
Best Local Similarity   100.0%; Pred. No. 1.6e-25;
Matches   40; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 4
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 1251 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10020
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/486,596A
;   FILING DATE: JUNE 7, 1995
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 596-9000
;   TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 185 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-486-596A-1

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Query Match           100.0%;  Score 219; DB 2;  Length 185;
Best Local Similarity 100.0%;  Pred. No. 1.6e-25;
Matches  40; Conservative   0; Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        ||||||||||||||||||||||||||||||||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 5
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: c/o FISH & NEAVE
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10020
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/004,713
;     FILING DATE: JANUARY 7, 1998
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: HALEY Jr., James F.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 596-9000
;     TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 185 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-004-713-1

Query Match           100.0%;  Score 219; DB 2;  Length 185;
Best Local Similarity 100.0%;  Pred. No. 1.6e-25;
Matches  40; Conservative   0; Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        ||||||||||||||||||||||||||||||||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 6
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: c/o FISH & NEAVE
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10020
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/233,389C
;     FILING DATE: 26-APR-1994
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: HALEY Jr., James F.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: SHGN-5
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 596-9000
;     TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3: .
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 188 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-233-389C-3

Query Match            97.3%;  Score 213; DB 1;  Length 188;
Best Local Similarity  97.5%;  Pred. No. 1.3e-24;
Matches  39; Conservative   0; Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        |||||||||||||||||||||||||| |||| |||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 7
US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: c/o FISH & NEAVE
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10020
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/801,863
;     FILING DATE: CONCURRENTLY HEREWITH
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: HALEY Jr., James F.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 596-9000
;     TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
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;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 188 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-801-863-3

Query Match      97.3%;  Score 213;  DB 2;  Length 188;
Best Local Similarity 97.5%;  Pred. No. 1.3e-24;
Matches  39;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 SFGCRFGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         |||||||||||||||||||||||||||||| |||||||||||
Db  107 SFGCRFGCTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 8
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: c/o FISH & NEAVE
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10020
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/486,596A
;     FILING DATE: JUNE 7, 1995
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: HALEY Jr., James F.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 596-9000
;     TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 188 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-486-596A-3

Query Match      97.3%;  Score 213;  DB 2;  Length 188;
Best Local Similarity 97.5%;  Pred. No. 1.3e-24;
Matches  39;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 SFGCRFGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         |||||||||||||||||||||||||||||| |||||||||||
Db  107 SFGCRFGCTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 9
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
;   APPLICANT: KITAMURA, Kazuo
;   APPLICANT: KANGAWA, Kenji
;   APPLICANT: MATSUO, Hisayuki
;   APPLICANT: ETO, Tanenao
;   TITLE OF INVENTION: ADRENOMEDULLIN
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: c/o FISH & NEAVE
;     STREET: 1251 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10020
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/004,713
;     FILING DATE: JANUARY 7, 1998
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: HALEY Jr., James F.
;     REGISTRATION NUMBER: 27,794
;     REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 596-9000
;     TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 188 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-004-713-3

Query Match      97.3%;  Score 213;  DB 2;  Length 188;
Best Local Similarity 97.5%;  Pred. No. 1.3e-24;
Matches  39;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 SFGCRFGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         |||||||||||||||||||||||||||||| |||||||||||
Db  107 SFGCRFGCTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;   APPLICANT: Smith, Derek D.
;   APPLICANT: Saha, Shankar
;   APPLICANT: Abel, Peter W.
;   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;   TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;     STREET: 119 No. 6268474th Fourth Street
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55401
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/070,504
;     FILING DATE: 30-APR-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
```

```
;         NAME: McCormack, Myra H
;         REGISTRATION NUMBER: 36,602
;         REFERENCE/DOCKET NUMBER: 180.00020101
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 612/305-1220
;         TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 50 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-09-070-504-15

Query Match             89.5%;  Score 196;  DB 4;  Length 50;
Best Local Similarity   87.5%;  Pred. No. 1e-22;
Matches    35;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
            | |||||||||||||||||||||||||| :|||:|:||||||
Db       11 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 50


RESULT 11
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
;     APPLICANT: Smith, Derek D.
;     APPLICANT: Saha, Shankar
;     APPLICANT: Abel, Peter W.
;     TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;     TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
;     NUMBER OF SEQUENCES: 23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;       STREET: 119 No. 6268474th Fourth Street
;       CITY: Minneapolis
;       STATE: MN
;       COUNTRY: USA
;       ZIP: 55401
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/070,504
;       FILING DATE: 30-APR-1998
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME: McCormack, Myra H
;       REGISTRATION NUMBER: 36,602
;       REFERENCE/DOCKET NUMBER: 180.00020101
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 612/305-1220
;       TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 23:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 31 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-09-070-504-23

Query Match             74.4%;  Score 163;  DB 4;  Length 31;
Best Local Similarity   100.0%;  Pred. No. 5.6e-18;
Matches    31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
            |||||||||||||||||||||||||||||||
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```
Db        1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 12
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
;     APPLICANT: Cuttitta, Frank; Martinez,
;     APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
;     APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
;     APPLICANT: Karen; Macri, Charles
;     TITLE OF INVENTION: Functional Role of
;     TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
;     TITLE OF INVENTION: Product (PAMP) in Human Pathology and
;     TITLE OF INVENTION: Physiology
;     NUMBER OF SEQUENCES: 17
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;       STREET: 345 Park Avenue
;       CITY: New York
;       STATE: NY
;       COUNTRY: USA
;       ZIP: 10154-0053
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy Disk
;       COMPUTER: IBM PC Compatible
;       OPERATING SYSTEM: MS WORD 97
;       SOFTWARE: ASCII
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/011,922A
;       FILING DATE: 17-Feb-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/60/002,514
;       FILING DATE: 18-Aug-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/60/002,936
;       FILING DATE: 30-Aug-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/60/013,172
;       FILING DATE: 12-Mar-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: PCT/US96/13286
;       FILING DATE: 16-Aug-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Leslie A. Serunian
;       REGISTRATION NUMBER: 35,353
;       REFERENCE/DOCKET NUMBER: 2026-4202US3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 758-4800
;       TELEFAX: (212) 751-6849
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 31 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     FEATURE:
;       NAME/KEY: P072
;       OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Query Match             74.4%;  Score 163;  DB 4;  Length 31;
Best Local Similarity   100.0%;  Pred. No. 5.6e-18;
Matches    31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
            |||||||||||||||||||||||||||||||
Db        1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 13
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US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
  APPLICANT: Cuttitta, Frank; Martinez,
  APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
  APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
  APPLICANT: Karen; Macri, Charles
  TITLE OF INVENTION: Functional Role of
  TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
  TITLE OF INVENTION: Product (PAMP) in Human Pathology and
  TITLE OF INVENTION: Physiology
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
  STREET: 345 Park Avenue
  CITY: New York
  STATE: NY
  COUNTRY: USA
  ZIP: 10154-0053
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy Disk
  COMPUTER: IBM PC Compatible
  OPERATING SYSTEM: MS WORD 97
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/011,922A
  FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,514
  FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,936
  FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/013,172
  FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US96/13286
  FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Leslie A. Serunian
  REGISTRATION NUMBER: 35,353
  REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 758-4800
  TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
  LENGTH: 31 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  HYPOTHETICAL: NO
  FEATURE:
  OTHER INFORMATION: Synthetic homolog of
  OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Query Match   74.4%;- Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches   31; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        |||||||||||||||||||||||||||||||
Db   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 14
US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:

US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
  APPLICANT: Cuttitta, Frank; Martinez,
  APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
  APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
  APPLICANT: Karen; Macri, Charles
  TITLE OF INVENTION: Functional Role of
  TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
  TITLE OF INVENTION: Product (PAMP) in Human Pathology and
  TITLE OF INVENTION: Physiology
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
  STREET: 345 Park Avenue
  CITY: New York
  STATE: NY
  COUNTRY: USA
  ZIP: 10154-0053
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy Disk
  COMPUTER: IBM PC Compatible
  OPERATING SYSTEM: MS WORD 97
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/011,922A
  FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,514
  FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/002,936
  FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/013,172
  FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US96/13286
  FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Leslie A. Serunian
  REGISTRATION NUMBER: 35,353
  REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 758-4800
  TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  LENGTH: 13 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  HYPOTHETICAL: NO
  FEATURE:
  NAME/KEY: P071
  OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2

Query Match   26.0%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 16 HQIYQFTDKD 25
        ||||||||||
Db   4 HQIYQFTDKD 13

RESULT 15
US-08-966-388-4
; Sequence 4, Application US/08966388
; Patent No. 5965412
; GENERAL INFORMATION:
  APPLICANT: Tomoyuki NISHIMOTO
  APPLICANT: Michio KUBOTA
  APPLICANT: Hiroto CHAEN
  APPLICANT: Toshio MIYAKE

```
..;    TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
..;    NUMBER OF SEQUENCES:  10
..;    CORRESPONDENCE ADDRESS:
..;      ADDRESSEE:  BROWDY AND NEIMARK
..;      STREET:  419 Seventh Street, N.W., Suite 300
..;      CITY:  Washington
..;      STATE:  D.C.
..;      COUNTRY:  USA
..;      ZIP:  20004
..;    COMPUTER READABLE FORM:
..;      MEDIUM TYPE:  Floppy disk
..;      COMPUTER:  IBM PC compatible
..;      OPERATING SYSTEM:  PC-DOS/MS-DOS
..;      SOFTWARE:  Patent In Release #1.0, Version #1.30
..;    CURRENT APPLICATION DATA:
..;      APPLICATION NUMBER:  US/08/966,388
..;      FILING DATE:
..;      CLASSIFICATION:  435
..;    PRIOR APPLICATION DATA:
..;      APPLICATION NUMBER:  JP 311,235/1996
..;      FILING DATE:  8-NOV-1996
..;    PRIOR APPLICATION DATA:
..;      APPLICATION NUMBER:  JP 61,710/97
..;      FILING DATE:  3-MAR-1997
..;    ATTORNEY/AGENT INFORMATION:
..;      NAME:  BROWDY, Roger L.
..;      REGISTRATION NUMBER:  25,618
..;      REFERENCE/DOCKET NUMBER:
..;    TELECOMMUNICATION INFORMATION:
..;      TELEPHONE:  202-628-5197
..;      TELEFAX:  202-737-3528
..;      TELEX:  248633
..;    INFORMATION FOR SEQ ID NO:  4:
..;      SEQUENCE CHARACTERISTICS:.
..;      LENGTH:  775 amino acids
..;      TYPE:  amino acid
..;      TOPOLOGY:  linear
..;      MOLECULE TYPE:  peptide
US-08-966-388-4

Query Match          23.7%;    Score 52;  DB 2;  Length 775;
Best Local Similarity  36.0%;    Pred. No. 15;
Matches     9;  Conservative    7;  Mismatches    9;  Indels   0;  Gaps   0;

Qy     15 AHQIYQFTDKDKDNVAPRSKISPQG 39
             | :::| : ||:|::|  : | |
Db    217 AVRLYHYEDKEKNNIAKFKRFLPLG 241

Search completed: October 17, 2002, 14:48:42
Job time : 5.49127 secs
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          GenCore version 5.1.3
     Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 17, 2002, 14:45:20 ; Search time 12.5786 Seconds
                                          (without alignments)
                                          459.181 Million cell updates/sec

Title:          US-10-018-924-2_COPY_95_146
Perfect score:  283
Sequence:       1 YRQSMNNFQGLRSFGCRFGT.........FTDKDKDNVAPRSKISPQGY 52

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters:    747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      2:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
      3:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
      4:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
      5:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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      7:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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     10:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
     11:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
     12:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
     13:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
     14:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
     15:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
     16:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
     17:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
     18:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
     19:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
     20:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
     21:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
     22:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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Pred. No. is the number of results, predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	283	100.0	52	22	AAB75110	Human adrenomedull
2	283	100.0	52	22	AAB91759	Adrenomedullin pep
3	283	100.0	52	22	AAE09818	Human adrenomedull
4	283	100.0	53	22	AAB75111	Glycine extended h
5	283	100.0	53	22	AAB75112	Glycine extended a
6	283	100.0	62	22	AAB75113	Linker peptide-adr
7	283	100.0	120	22	AAB75122	UspA(1-57)-(A)-(GS
8	283	100.0	120	22	AAB75123	UspA(1-56)-(DD)-(G
9	283	100.0	147	22	AAB75124	UspA(1-84)-(A)-(GS
10	283	100.0	170	22	AAB75114	Thioredoxin-(GSGSG
11	283	100.0	185	22	AAB49697	Human adrenomedull
12	283	100.0	185	22	AAB60344	Human adrenomedull
13	277	97.9	188	22	AAB49698	Porcine adrenomedu
14	277	97.9	188	22	AAB60345	Porcine adrenomedu
15	231	81.6	50	22	AAE09819	Rat adrenomedullin
16	231	81.6	185	22	AAB49699	Rat adrenomedullin
17	231	81.6	185	22	AAB60346	Rat adrenomedullin
18	227	80.2	52	22	AAB91765	Adrenomedullin pep
19	219.5	77.6	53	22	AAB91767	Adrenomedullin pep
20	196	69.3	40	22	AAB91768	Adrenomedullin pep
21	181.5	64.1	37	22	AAB91761	Adrenomedullin pep
22	163	57.6	31	18	AAW25160	Human preproadreno
23	163	57.6	31	22	AAB91762	Adrenomedullin pep
24	163	57.6	31	22	AAE09827	Human adrenomedull
25	64	22.6	12	22	AAB91760	Adrenomedullin pep
26	61	21.6	1541	18	AAW33361	Rat canalicular mu
27	60	21.2	231	21	AAB11449	Human cMOAT C-term
28	60	21.2	231	21	AAB28224	Multi-drug resista
29	60	21.2	1545	18	AAW33362	Human canalicular
30	59	20.8	1545	19	AAW55966	Human canalicular
31	57	20.1	13	18	AAW25159	Human preproadreno
32	56.5	20.0	1346	22	ABB65953	Drosophila melanog
33	56	19.8	339	21	AAB26100	Mycobacterium auru
34	56	19.8	339	21	AAB26104	Mycobacterium auru
35	56	19.8	500	21	ABB67015	Drosophila melanog
36	56	19.8	858	15	AAR53404	S-Locus receptor (
37	56	19.8	858	19	AAW49080	Brassica sp. S-rec
38	56	19.8	1302	21	ABB65954	Drosophila melanog
39	55	19.4	297	22	AAY75592	Neisseria gonorrhe
40	55	19.4	1344	22	ABB59224	Drosophila melanog
41	54.5	19.3	482	21	AAG14118	Arabidopsis thalia
42	54.5	19.3	482	21	AAG54151	Arabidopsis thalia
43	54.5	19.3	483	21	AAG14117	Arabidopsis thalia
44	54.5	19.3	483	21	AAG54150	Arabidopsis thalia
45	54.5	19.3	490	21	AAG54149	Arabidopsis thalia

ALIGNMENTS

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RESULT 1
AAB75110
ID   AAB75110 standard; protein;  52 AA.
XX
AC   AAB75110;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Human adrenomedullin (AM) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A,  Mitsuda Y,  Nakayama T,  Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19806.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
```

PS Disclosure; Page 45; 75pp; Japanese.
XX
CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic application. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 52 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 52;
Best Local Similarity 100.0%;   Pred. No. 2.6e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 2
AAB91759
ID AAB91759 standard; Peptide; 52 AA.
XX
AC AAB91759;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999;   99US-0134406.
PR 10-SEP-1999;   99US-0153406.
PR 15-OCT-1999;   99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 498; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 52 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 52;
Best Local Similarity 100.0%;   Pred. No. 2.6e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 3
AAE09818
ID AAE09818 standard; peptide; 52 AA.
XX
AC AAE09818;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human adrenomedullin peptide #1.
XX
KW Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.
XX
OS Homo sapiens.
XX
PN US6268474-B1.
XX
PD 31-JUL-2001.
XX
PF 30-APR-1998;   98US-0070504.
XX
PR 30-APR-1998;   98US-0070504.
XX
PA (UYCR-) UNIV CREIGHTON.
XX
PI Smith DD, Saha S, Abel PW;
XX
DR WPI; 2001-564216/63.
XX
PT Vasoactive peptides useful for inhibiting calcitonin gene related
PT peptide receptor activity -
XX
PS Claim 5; Column 25-26; 24pp; English.
XX
CC The invention relates to antagonists of the vasoactive peptide
CC calcitonin gene related peptide (CGRP) and other members of the
CC CGRP superfamily. The invention also relates to amino the terminal
CC modifications of peptides to improve their ability to bind to a
CC member of the CGRP-receptor super-family. CGRP antagonists are
CC used for inhibiting CGRP activity which can be used in vitro e.g.
CC in assays to identify and/or isolate CGRP receptors or with intact
CC cells either in vitro or in vivo to inhibit the effect of CGRP
CC binding to its receptor. The present sequence is human
CC adrenomedullin peptide.
XX
SQ Sequence 52 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 52;
Best Local Similarity 100.0%;   Pred. No. 2.6e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

```
RESULT 4
AAB75111
ID   AAB75111 standard; Protein; 53 AA.
XX
AC   AAB75111;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Glycine extended human adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19807.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Example 1; Page 46; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  53 AA;

Query Match             100.0%;  Score 283; DB 22;  Length 53;
Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
Matches    52; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 5
AAB75112
ID   AAB75112 standard; Protein; 53 AA.
XX
AC   AAB75112;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Glycine extended adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19808.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 47; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  53 AA;

Query Match             100.0%;  Score 283; DB 22;  Length 53;
Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
Matches    52; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 6
AAB75113
ID   AAB75113 standard; Protein; 62 AA.
XX
AC   AAB75113;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Linker peptide-adrenomedullin (AM) precursor protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19809.
```

XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 20; Page 48; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   62 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 62;
Best Local Similarity 100.0%;   Pred. No. 3.3e-32;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 61

RESULT 7
AAB75122
ID   AAB75122 standard; Protein; 120 AA.
XX
AC   AAB75122;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19864.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 68; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the

CC   exemplification of the present invention.
XX
SQ   Sequence   120 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 120;
Best Local Similarity 100.0%;   Pred. No. 7.1e-32;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119

RESULT 8
AAB75123
ID   AAB75123 standard; Protein; 120 AA.
XX
AC   AAB75123;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19865.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 69-70; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   120 AA;

Query Match   100.0%;   Score 283; DB 22;   Length 120;
Best Local Similarity 100.0%;   Pred. No. 7.1e-32;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119

RESULT 9
AAB75124

```
ID   AAB75124 standard; Protein; 147 AA.
XX
AC   AAB75124;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19866.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 71; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   147 AA;

  Query Match             100.0%;  Score 283;  DB 22;  Length 147;
  Best Local Similarity   100.0%;  Pred. No. 9e-32;
  Matches   52;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 10
AAB75114
ID   AAB75114 standard; Protein; 170 AA.
XX
AC   AAB75114;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Thioredoxin-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19810.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 49-50; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   170 AA;

  Query Match             100.0%;  Score 283;  DB 22;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-31;
  Matches   52;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169

RESULT 11
AAB49697
ID   AAB49697 standard; Protein; 185 AA.
XX
AC   AAB49697;
XX
DT   04-APR-2001 (first entry)
XX
DE   Human adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; human.
XX
OS   Homo sapiens.
XX
PN   WO20007838-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999; 99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29138.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle -
PT   comprises adrenomedullin
```

```
XX
PS    Claim 1; Page 26-27; 42pp; Japanese.
XX
CC    This invention relates to a composition for promoting passive elongation
CC    of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC    uropathic activity. The composition can be used for promoting passive
CC    elongation of vesicle smooth muscles, this is useful for relieving
CC    urinary disorders such as impending urinary incontinence, reflex urinary
CC    incontinence and urinary incontinence with overflow. The present sequence
CC    represents the human adrenomedullin protein, which is used in the
CC    composition of the invention.
XX
SQ    Sequence   185 AA;

Query Match             100.0%;  Score 283; DB 22; Length 185;
Best Local Similarity   100.0%;  Pred. No. 1.2e-31;
  Matches  52;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 12
AAB60344
ID    AAB60344 standard; Protein; 185 AA.
XX
AC    AAB60344;
XX
DT    06-APR-2001 (first entry)
XX
DE    Human adrenomedullin precursor.
XX
KW    Human; adrenomedullin; precursor; bradykinin antagonist;
KW    uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW    dysmenorrhoea; obstetric; gynaecological.
XX
OS    Homo sapiens.
XX
PN    WO200078339-A1.
XX
PD    28-DEC-2000.
XX
PF    23-JUN-2000; 2000WO-JP04167.
XX
PR    23-JUN-1999;  99JP-0177548.
PR    21-MAR-2000; 2000JP-0079171.
XX
PA    (SHIO ) SHIONOGI & CO LTD.
XX
PI    Yanagita T;
XX
DR    WPI; 2001-080755/09.
DR    N-PSDB; AAF27228.
XX
PT    Composition for inhibiting automatic uterine contraction or contraction
PT    caused by bradykinin comprises adrenomedullin -
XX
PS    Claim 7; Page 37-38; 54pp; Japanese.
XX
CC    The invention relates to a composition containing adrenomedullin for
CC    inhibiting automatic uterine contraction or contraction caused by
CC    bradykinin. The invention also relates to the use of adrenomedullin in
CC    the preparation of a drug for preventing premature birth or miscarriage.
CC    The composition of the invention can be used for preventing premature
CC    birth, preventing miscarriage, stopping delivery before caesarean
CC    section or for treating dysmenorrhoea. The present sequence
CC    represents human adrenomedullin precursor.
XX
SQ    Sequence   185 AA;

Query Match             100.0%;  Score 283; DB 22; Length 185;
Best Local Similarity   100.0%;  Pred. No. 1.2e-31;
```

```
Matches  52;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 13
AAB49698
ID    AAB49698 standard; Protein; 188 AA.
XX
AC    AAB49698;
XX
DT    04-APR-2001 (first entry)
XX
DE    Porcine adrenomedullin amino acid sequence.
XX
KW    Passive elongation; vesicle smooth muscle; uropathic activity;
KW    adrenomedullin; urinary disorder; incontinence; procine.
XX
OS    Sus scrofa.
XX
PN    WO200078338-A1.
XX
PD    28-DEC-2000.
XX
PF    23-JUN-2000; 2000WO-JP04166.
XX
PR    23-JUN-1999;  99JP-0177549.
XX
PA    (SHIO ) SHIONOGI & CO LTD.
XX
PI    Yanagita T;
XX
DR    WPI; 2001-080754/09.
DR    N-PSDB; AAF29139.
XX
PT    Composition for promoting passive elongation of vesicle smooth muscle
PT    comprises adrenomedullin -
XX
PS    Disclosure; Page 31-33; 42pp; Japanese.
XX
CC    This invention relates to a composition for promoting passive elongation
CC    of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC    uropathic activity. The composition can be used for promoting passive
CC    elongation of vesicle smooth muscles, this is useful for relieving
CC    urinary disorders such as impending urinary incontinence, reflex urinary
CC    incontinence and urinary incontinence with overflow. The present sequence
CC    represents the porcine adrenomedullin protein, which is used in the
CC    composition of the invention.
XX
SQ    Sequence   188 AA;

Query Match              97.9%;  Score 277; DB 22; Length 188;
Best Local Similarity    98.1%;  Pred. No. 8.4e-31;
Matches  51;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDGVAPRSKISPQGY 146


RESULT 14
AAB60345
ID    AAB60345 standard; Protein; 188 AA.
XX
AC    AAB60345;
XX
DT    06-APR-2001 (first entry)
XX
DE    Porcine adrenomedullin precursor.
XX
KW    Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
```

```
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Sus scrofa.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999;   99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27229.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Disclosure; Page 43-44; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents porcine adrenomedullin precursor.
XX
SQ   Sequence   188 AA;

Query Match      97.9%;   Score 277; DB 22;   Length 188;
Best Local Similarity  98.1%;   Pred. No. 8.4e-31;
Matches   51; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        ||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 15
AAE09819
ID   AAE09819 standard; peptide; 50 AA.
XX
AC   AAE09819;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Rat adrenomedullin peptide.
XX
KW   Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW   CGRP-receptor identification; adrenomedullin.
XX
OS   Rattus sp.
XX
PN   US6268474-B1.
XX
PD   31-JUL-2001.
XX
PF   30-APR-1998;   98US-0070504.
XX
PR   30-APR-1998;   98US-0070504.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Smith DD, Saha S, Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related
PT   peptide receptor activity -
XX
PS   Claim 5; Column 25-26; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide
CC   calcitonin gene related peptide (CGRP) and other members of the
CC   CGRP superfamily. The invention also relates to amino the terminal
CC   modifications of peptides to improve their ability to bind to a
CC   member of the CGRP-receptor super-family. CGRP antagonists are
CC   used for inhibiting CGRP activity which can be used in vitro e.g.
CC   in assays to identify and/or isolate CGRP receptors or with intact
CC   cells either in vitro or in vivo to inhibit the effect of CGRP
CC   binding to its receptor. The present sequence is rat adrenomedullin
CC   peptide.
XX
SQ   Sequence   50 AA;

Query Match      81.6%;   Score 231; DB 22;   Length 50;
Best Local Similarity  84.6%;   Pred. No. 5.1e-25;
Matches   44; Conservative   3; Mismatches   3; Indels   2; Gaps   1;

Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        |||||| || || |||||||||:||||||||||||||| :||:|||||||
Db    1 YRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 50

Search completed: October 17, 2002, 14:47:59
Job time : 12.5786 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 5.96509 Seconds
                                 (without alignments)
                                 837.648 Million cell updates/sec

Title: US-10-018-924-2_COPY_95_146
Perfect score: 283
Sequence: 1 YRQSMNNFQGLRSFGCRFGT.........FTDKDKDNVAPRSKISPQGY 52
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_71:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	283	100.0	185	2	JN0684	adrenomedullin pre
2	277	97.9	188	2	S41600	adrenomedullin - p
3	231	81.6	185	2	JN0766	adrenomedullin pre
4	65.5	23.1	532	2	JC1392	monophenol monooxy
5	61.5	21.7	430	2	T14536	S-locus-specific g
6	61	21.6	1541	1	S71839	canalicular multid
7	60.5	21.4	253	2	H81690	conserved hypothet
8	59	20.8	1545	1	S71841	multidrug resistan
9	58.5	20.7	189	2	A99638	hypothetical prote
10	58.5	20.7	189	2	A85489	hypothetical prote
11	58.5	20.7	431	2	T14415	S-locus-specific g
12	57.5	20.3	429	2	T07809	S-receptor kinase
13	57	20.3	712	2	AG2058	ABC transporter AT
14	57	20.1	273	2	PC4153	monophenol monooxy
15	56	19.8	428	2	T14529	S-locus-specific g
16	56	19.8	858	1	JQ1677	S-receptor kinase
17	55.5	19.6	373	2	G84107	lipopolysaccharide
18	55.5	19.6	465	2	T15540	hypothetical prote
19	55	19.4	319	2	S20799	histidine--tRNA li
20	55	19.4	444	1	E69104	hypothetical prote
21	54.5	19.3	93	2	E91004	hypothetical prote
22	54.5	19.3	93	2	E85637	hypothetical prote
23	54.5	19.3	428	2	T07814	S-locus-specific g
24	54.5	19.3	436	2	A27827	S-locus-specific g
25	54.5	19.3	463	2	T46165	pectate lyase-like
26	54	19.1	370	2	T05598	hypothetical prote
27	54	19.1	429	2	T14533	S-locus-specific g
28	53.5	18.9	107	2	H84839	late embryogenesis
29	53.5	18.9	358	2	H95398	probable ABC trans
30	53.5	18.9	362	2	B83963	hypothetical prote
31	53.5	18.9	427	2	T14424	S-locus-specific g
32	53.5	18.9	428	2	T14423	S-locus-specific g
33	53.5	18.9	617	2	T23197	hypothetical prote
34	53	18.7	151	2	C82867	virulence-associat
35	53	18.7	522	2	G86259	protein T12C24.12
36	53	18.7	529	1	YRHU1	monophenol monooxy
37	53	18.7	672	1	KIHUCA	protein kinase C (
38	53	18.7	672	1	KIRTC	protein kinase C (
39	53	18.7	672	1	KIMSCA	protein kinase C (
40	53	18.7	672	1	KIRBC	protein kinase C (
41	53	18.7	672	1	KIBOC	protein kinase C (
42	53	18.7	676	2	A37237	protein kinase C (
43	53	18.7	2374	2	T21052	hypothetical prote
44	52.5	18.6	428	2	T14416	S-locus-specific g
45	52.5	18.6	428	2	T14530	S-locus-specific g

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:9354869
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys.Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A;Reference number: JN0684; MUID:9343928
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A;Reference number: JN0476; MUID:9249425
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Accession: PN0548
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Product: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match   100.0%;   Score 283; DB 2;   Length 185;
Best Local Similarity 100.0%;   Pred. No. 4.7e-30;
Matches   52; Conservative   0; Mismatches   0;   Indels   0;   Gaps   0;

```
Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
```

RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA enco
A;Reference number: S41600; MUID:94139945
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

Query Match   97.9%;   Score 277; DB 2; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-29;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
```

RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

Query Match   81.6%;   Score 231; DB 2; Length 185;
Best Local Similarity 84.6%; Pred. No. 3.8e-23;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

```
Qy    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
        ||||| || |||||||||||||||||||||||||||||||| :||:||||||
Db   94 YRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDGMAPRNKISPQGY 143
```

RESULT 4
JC1392
monophenol monooxygenase (EC 1.14.18.1) - Japanese pond frog
N;Alternate names: tyrosinase
C;Species: Rana nigromaculata (Japanese pond frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JC1392; I51169
R;Takase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishioka, M.
Gene 121, 359-363, 1992
A;Title: Cloning and sequencing of the cDNA encoding tyrosinase of Japanese pond frog
A;Reference number: JC1392; MUID:93077054
A;Accession: JC1392
A;Molecule type: mRNA
A;Residues: 1-532 <TAK>
A;Cross-references: DDBJ:D12514; NID:g222946; PIDN:BAA02077.1; PID:g222947
R;Miura, I.; Okumoto, H.; Makino, K.; Nakata, A.; Nishioka, M.
Jpn.J. Genet. 70, 79-92, 1995
A;Title: Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculat
A;Reference number: I51169; MUID:95290234
A;Accession: I51169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9, A',11-277 <MIU>
A;Cross-references: GB:D37779; NID:g809507; PIDN:BAA07034.1; PID:g809508
C;Superfamily: monophenol monooxygenase
C;Keywords: glycoprotein; oxidoreductase; transmembrane protein
F;47,90,115,165,234,294,341,360,375/Binding site: carbohydrate (Asn) (covalent) #stat

Query Match   23.1%;   Score 65.5; DB 2; Length 532;
Best Local Similarity 33.9%; Pred. No. 1.2;
Matches 20; Conservative 8; Mismatches 18; Indels 13; Gaps 4;

```
Qy    3 QSMNNFQGLRSFGCREG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 49
          | | ||| ||  | :    |:| :|     |:| || ::|          ||||||
Db   94 QCQGNFMGYNCGECRFGYTGPNCTVRRNMIRKDIFRMTTAEKDKLIAYLNLA-KHTISP 151
```

RESULT 5
T14536
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-430 <KUS>
C;Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
C;Superfamily: S-locus-specific glycoprotein; s-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   21.7%;   Score 61.5; DB 2; Length 430;
Best Local Similarity 28.6%; Pred. No. 3.2;
Matches 14; Conservative 12; Mismatches 12; Indels 11; Gaps 2;

```
Qy   15 GCRF-GTCTVQKLAHQIYQFTDKDKD-------NVAPRSKISPQGY 52
         ||| | ||: ||    :|   |: :|        : ||| ||
Db  220 GIRFSGIPEDEKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268
```

RESULT 6
S71839
canalicular multidrug resistance protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71839
R;Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler,
J. Biol. Chem. 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan
A;Reference number: S71839; MUID:96279006
A;Accession: S71839
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1541 <BUE>

A;Cross-references: EMBL:X96393; NID:g1292881; PIDN:CAA65257.1; PID:g1617207
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;100-124/Domain: transmembrane #status predicted <TM01>
F;127-151/Domain: transmembrane #status predicted <TM02>
F;160-187/Domain: transmembrane #status predicted <TM03>
F;305-329/Domain: transmembrane #status predicted <TM04>
F;354-381/Domain: transmembrane #status predicted <TM05>
F;431-451/Domain: transmembrane #status predicted <TM06>
F;456-476/Domain: transmembrane #status predicted <TM07>
F;536-564/Domain: transmembrane #status predicted <TM08>
F;574-602/Domain: transmembrane #status predicted <TM09>
F;650-833/Domain: ATP-binding cassette homology <ABC1>
F;667-674/Region: nucleotide-binding motif A (P-loop)
F;966-994/Domain: transmembrane #status predicted <TM10>
F;1018-1046/Domain: transmembrane #status predicted <TM11>
F;1104-1132/Domain: transmembrane #status predicted <TM12>
F;1203-1228/Domain: transmembrane #status predicted <TM13>
F;1313-1506/Domain: ATP-binding cassette homology <ABC2>
F;1330-1337/Domain: nucleotide-binding motif A (P-loop)
F;6.1007.1010.1011/Binding site: carbohydrate (Asn) (Covalent) #status predicted

Query Match   21.6%; Score 61; DB 1; Length 1541;
Best Local Similarity 38.2%; Pred. No. 14;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy   18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 51
          ||| ||| :|::::|| | |||| | |
Db   1479 FSQCTVITIAHRLHTIMDSDKIMVLDNGKIVEYG 1512

RESULT 7
H81690
conserved hypothetical protein frameshift TC0556 [imported] - Chlamydia muridarum (strai
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
A;Accession: H81690
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID: 20150255
A;Accession: H81690
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <TET>
A;Cross-references: GB:AE002323; GB:AE002160; NID:g7190585; PIDN:AAF39395.1; PID:g7190059
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0556

Query Match   21.4%; Score 60.5; DB 2; Length 253;
Best Local Similarity 32.8%; Pred. No. 2.5;
Matches 22; Conservative 8; Mismatches 22; Indels 15; Gaps 4;

Qy   1 YRQSMNNF------QG--LRSFGCR-----FGTCTVQKLAHQIYQFTDKDKDNVA-PRS 45
          || || :| :| :| ::| ||| ||| |:|
Db   186 YRRQMFNLPVDGSLAQGRDLRLFGYRNIKDWFGDRYVSAVTEAVLRFIDEQKKNIAMPSL 245

Qy   46 KISPQG 52
          | ||
Db   246 KEAQQDF 252

RESULT 8
S71841
multidrug resistance protein, canalicular - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71841; S71840
R;Koenig, J.; Keppler, D.
submitted to the EMBL Data Library, August 1996
A;Reference number: S71841

A;Accession: S71841
A;Molecule type: mRNA
A;Residues: 1-1545 <KOE>
R;Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler,
J. Biol. Chem. 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan
A;Reference number: S71839; MUID:9627906
A;Accession: S71840
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1415-1429,'VP',1432-1455,'E',1457-1545 <BUE>
A;Cross-references: EMBL:X96395
C;Genetics:
A;Gene: GDB:ABCC2; CMOAT; ABC; MRP2; CMRP; DJS
A;Cross-references: GDB:6089489; OMIM:601107
A;Map position: 10q24-10q24
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homolo
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;654-837/Domain: ATP-binding cassette homology <ABC1>
F;671-678/Region: nucleotide-binding motif A (P-loop)
F;1317-1510/Domain: ATP-binding cassette homology <ABC2>
F;1334-1341/Region: nucleotide-binding motif A (P-loop)

Query Match   20.8%; Score 59; DB 1; Length 1545;
Best Local Similarity 37.8%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy   18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 50
          ||| ||| :|::::|| | | ||
Db   1483 FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSPE 1519

RESULT 9
A99638
hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: A99638
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:g13359529; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0073
C;Superfamily: Escherichia coli yabP protein

Query Match   20.7%; Score 58.5; DB 2; Length 189;
Best Local Similarity 34.4%; Pred. No. 3.4;
Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

Qy   25 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 51
          || |:|:| ::||:|
Db   95 KLTHWLKFNELKEYAKDPENMAAKASLSPEG 126

RESULT 10
A85489
hypothetical protein Z0078 [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A85489
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <STO>
A;Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:200
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0078
C;Superfamily: Escherichia coli yabP protein

Query Match   20.7%; Score 58.5; DB 2; Length 189;
Best Local Similarity 34.4%; Pred. No. 3.4;
Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

Qy   25 KLAHQIYQFTD----KDKDNVAPRSKISPQG 51
         ||·||·:|| ||·|||·|·:||:|
Db   95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126

RESULT 11
T14415
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14415
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
echanism.
A;Reference number: T14415
A;Accession: T14415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <KUS>
A;Cross-references: EMBL:D85215; NID:g2351161; PIDN:BAA21949.1; PID:g2351162
C;Superfamily: S-locus specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   20.7%; Score 58.5; DB 2; Length 431;
Best Local Similarity 32.7%; Pred. No. 7.9;
Matches 16; Conservative 8; Mismatches 14; Indels 11; Gaps 2;

Qy   15 GCRF-GTCTVQKLAHQIYQFTDKD-------NVAPRSKISPQGY 52
         |·||| ||·|·|·|·:·|:||·:| ·: ·||·|||
Db   222 GVRFSGMPGCDQKLNYMVYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270

RESULT 12
T07809
S-receptor kinase (EC 2.7.1.-) - radish (fragment)
N;Alternate names: S glycoprotein
C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07809
R;Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A;Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related gen
A;Reference number: Z16146; MUID:98311079
A;Accession: T07809
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-429 <SAK>
A;Cross-references: EMBL:AB009677; NID:g3327839; PIDN:BAA31724.1; PID:g3327840
C;Genetics:
A;Gene: SLG(S1)
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: ATP; glycoprotein; magnesium; phosphotransferase; serine/threonine-specific
F;32-427/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match   20.3%; Score 57.5; DB 2; Length 429;
Best Local Similarity 30.0%; Pred. No. 11;

Matches 18; Conservative 10; Mismatches 15; Indels 17; Gaps 3;

Qy   10 GLRSF-----GCRF-GTCTVQKLAHQIYQFTDKD--------NVAPRSKISPQGY 52
         ||| ||| |·:·||| ··:: :: |||·|||
Db   209 GLRSHRSGPWNGIRFSGIPEDQKSSYMVYSFTENSEEVAYTFRMTNSSIYSRLKISSEGF 268

RESULT 13
AG2058
ABC transporter ATP-binding protein all2021 [imported] - Anabaena sp. (strain PCC 712
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AG2058
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-712 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73720.1; PID:g17131112; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2021

Query Match   20.3%; Score 57.5; DB 2; Length 712;
Best Local Similarity 37.2%; Pred. No. 18;
Matches 16; Conservative 6; Mismatches 16; Indels 5; Gaps 2;

Qy   9 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPQG 51
         ·||·|| || ··:: ||·|| |·|·:| ·| ·||||
Db   655 QNLRRRGC---TCII--VAHRLSTRDCDQIIVLERGKVVQQG 692

RESULT 14
PC4153
monophenol monooxygenase (EC 1.14.18.1) - chicken
N;Alternate names: tyrosinase
C;Species: Gallus gallus (chicken)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 18-Jun-1999
C;Accession: PC4153
R;Ferguson, C.A.; Kidson, S.H.
Gene 169, 191-195, 1996
A;Title: Characteristic sequences in the promoter region of the chicken tyrosinase-en
A;Reference number: PC4153; MUID:96194800
A;Accession: PC4153
A;Molecule type: DNA
A;Residues: 1-273 <FER>
A;Cross-references: GB:L46805; NID:g1146320; PIDN:AAB08441.1; PID:g1146321
A;Note: The DNA sequence includes the first exon and a part of the first intron
C;Comment: This enzyme is the rate-limiting enzyme in pigment biosynthesis.
C;Genetics:
A;Gene: ctyr4.3
C;Superfamily: monophenol monooxygenase
C;Keywords: oxidoreductase

Query Match   20.1%; Score 57; DB 2; Length 273;
Best Local Similarity 35.9%; Pred. No. 7.8;
Matches 14; Conservative 5; Mismatches 14; Indels 6; Gaps 2;

Qy   7 NFQGLRSFGCRFG---TCTVQKL-AHQIYQFTDKD 39
         ||·||··||| | ||·||·| ·||·|||||
Db   94 NFMGFNCGECKFGFSGQNCTERRLRTRRNIFQLTISEKD 132

RESULT 15
T14529
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14529
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
A;Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   19.8%;   Score 56; DB 2;   Length 428;
Best Local Similarity 31.1%;   Pred. No. 17;
Matches   19; Conservative   9; Mismatches   19; Indels   14; Gaps   3;

Qy   6 NNFQGLRS---FGCRF-GTCTVQKLAHQIYQFTDKDKD--------NVAPRSKISPQG 51
            : ||:|| | || | ||::| ||: .:| : | |:| |
Db   207 SGFQVHRSGPWNGVRFSGIPENQKLSYMVYNFTENSEEVAYTFRMTNNSFYSRLKVSSDG 266

Qy   52 Y 52
            |
Db   267 Y 267

Search completed: October 17, 2002, 14:46:18
Job time : 6.96509 secs

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                 GenCore version 5.1.3
         Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     October 17, 2002, 14:45:21 ; Search time 3.11222 seconds
                                         (without alignments)
                             646.939 Million cell updates/sec

Title:      US-10-018-924-2-COPY_95_146
Perfect score: 283
Sequence:   1 YRQSMNNFQGLRSFGCRFGT.........FTDKDKDNVAPRSKISPQGY 52

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:    105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_40:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	283	100.0	185	1	ADML_HUMAN	P35318 homo sapien
2	277	97.9	188	1	ADML_PIG	P53366 sus scrofa
3	265	93.6	188	1	ADML_CANFA	O77559 canis famil
4	263	92.9	188	1	ADML_BOVIN	O62827 bos taurus
5	231	81.6	185	1	ADML_RAT	P43145 rattus norv
6	222	78.4	184	1	ADML_MOUSE	P97297 mus musculu
7	65.5	23.1	532	1	TYRO_RANNI	Q04604 rana nigrom
8	61	21.6	1541	1	MRP2_RAT	Q63120 rattus norv
9	59	20.8	273	1	TYRO_COTJA	Q08410 coturnix co
10	59	20.8	1545	1	MRP2_HUMAN	Q92887 homo sapien
11	57	20.1	529	1	TYRO_CHICK	P55024 gallus gall
12	55	19.4	425	1	SYH_METTH	O26346 methanobact
13	55	19.4	1564	1	MRP2_RABIT	Q28689 oryctolagus
14	54.5	19.3	436	1	SLS6_BRAOL	P07761 brassica ol
15	53	18.7	529	1	TYRO_HUMAN	P14679 homo sapien
16	53	18.7	672	1	KPCA_BOVIN	P04409 bos taurus
17	53	18.7	672	1	KPCA_HUMAN	P17252 homo sapien
18	53	18.7	672	1	KPCA_MOUSE	P20444 mus musculu
19	53	18.7	672	1	KPCA_RABIT	P10102 oryctolagus
20	53	18.7	672	1	KPCA_RAT	P05696 rattus norv
21	52	18.4	273	1	TYRO_CANFA	P54834 canis famil
22	52	18.4	439	1	FGL2_HUMAN	Q14314 homo sapien
23	52	18.4	485	1	GATA_BACSU	O06491 bacillus su
24	51.5	18.2	305	1	LIGD_PSEPA	Q01198 pseudomonas
25	51.5	18.2	442	1	TOP5_BPT4	P07065 bacteriopha
26	51.5	18.2	1268	1	VGLN_HUMAN	Q00341 homo sapien
27	51	18.0	180	1	VG48_BPMU	Q9tlvi bacteriopha
28	51	18.0	273	1	TYRO_TRISI	P55026 trionyx sin
29	51	18.0	566	1	MXID_SHIFL	Q04641 shigella fl
30	51	18.0	566	1	MXID_SHISO	Q55293 shigella so
31	51	18.0	985	1	ENV_SFV1	P23073 simian foam
32	51	18.0	1325	1	MRP4_HUMAN	O15439 homo sapien
33	50.5	17.8	459	1	G33_RAT	P05432 rattus norv
34		50.5	17.8	805	1	FUSE_DROME	P23647 drosophila
35		50.5	17.8	922	1	YKF0_YEAST	P35736 saccharomyc
36		50	17.7	336	1	D3HI_HUMAN	P31937 homo sapien
37		50	17.7	354	1	1B24_HUMAN	P30470 homo sapien
38		50	17.7	362	1	1B35_HUMAN	P30477 homo sapien
39		50	17.7	399	1	GAL1_LACLA	Q9r7d7 lactococcus
40		50	17.7	573	1	EYA3_HUMAN	Q99504 homo sapien
41		50	17.7	1252	1	RPOB_CHLMU	P56869 chlamydia m
42		50	17.7	1252	1	RPOB_CHLPN	Q9za0 chlamydia p
43		50	17.7	1252	1	RPOB_CHLTR	O84317 chlamydia t
44		50	17.7	1319	1	SOS1_MOUSE	Q62245 mus musculu
45		50	17.7	1333	1	SOS1_HUMAN	Q07889 homo sapien

```
                        ALIGNMENTS

RESULT 1
ADML_HUMAN
ID    ADML_HUMAN     STANDARD;      PRT;   185 AA.
AC    P35318;
DT    01-FEB-1994 (Rel. 28, Created)
DT    01-FEB-1994 (Rel. 28, Last sequence update)
DT    16-OCT-2001 (Rel. 40, Last annotation update)
DE    ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE    terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN    ADM OR AM.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Pheochromocytoma;
RX    MEDLINE=93343928; PubMed=7688224;
RA    Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT    "Cloning and characterization of cDNA encoding a precursor for human
RT    adrenomedullin.";
RN    [2]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Liver;
RX    MEDLINE=94354869; PubMed=8074714;
RA    Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA    Kitamura K., Eto T., Matsuo H.;
RT    "Genomic structure of human adrenomedullin gene.";
RL    Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN    [3]
RP    SEQUENCE OF 95-146.
RC    TISSUE=Pheochromocytoma;
RX    MEDLINE=93249425; PubMed=8387282;
RA    Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA    Matsuo H., Eto T.;
RT    "Adrenomedullin: a novel hypotensive peptide isolated from human
RT    pheochromocytoma.";
RL    Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN    [4]
RP    REVIEW.
RX    MEDLINE=98240137; PubMed=9578982;
RA    Samson W.K.;
RT    "Proadrenomedullin-derived peptides.";
RL    Front. Neuroendocrinol. 19:100-127(1998).
RN    [5]
RP    REVIEW.
RX    MEDLINE=20053666; PubMed=10588445;
RA    Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT    "Structure-activity relationships of adrenomedullin in the circulation
RT    and adrenal gland.";
RL    Regul. Pept. 85:1-8(1999).
CC    -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC        AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
CC        PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
CC        KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
```

CC   INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC   PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC   INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC   AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
CC   ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC   VESSELS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
CC   ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC   TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   --
DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JN0476; JN0476.
DR   PIR; JN0684; JN0684.
DR   PIR; JC2351; JC2351.
DR   MIM; 103275; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92
FT   PEPTIDE   95   146   ADRENOMEDULLIN.
FT   PROPEP   148   185   PREPROAM C-TERMINAL FRAGMENT.
FT   DISULFID   110   115
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   185 AA;   20420 MW; 64C7D2A0B4654DFE CRC64;

Query Match   100.0%; Score 283; DB 1; Length 185;
Best Local Similarity   100.0%; Pred. No. 1.3e-30;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 YRQSMNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 YRQSMNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 2
ADML_PIG
ID   ADML_PIG   STANDARD;   PRT;   188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning
RT   of cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]

RP   SEQUENCE OF 22-41.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin
RT   N-terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC   AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC   KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; D14875; BAA03590.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92
FT   PEPTIDE   95   146   ADRENOMEDULLIN.
FT   PROPEP   153   188   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   110   115   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   188 AA;   20893 MW; 7174960F5660A61 CRC64;

Query Match   97.9%;   Score 277; DB 1; Length 188;
Best Local Similarity   98.1%;   Pred. No. 8.6e-30;
Matches   51; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 YRQSMNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 YRQSMNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 3
ADML_CANFA
ID   ADML_CANFA   STANDARD;   PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99002704; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).

CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC   AGENTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; AF045773; AAD05423.1; -.
DR EMBL; U96127; AAD09957.1; -.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL   1   21   BY SIMILARITY.
FT PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP   45   92   BY SIMILARITY.
FT PEPTIDE   95   146   ADRENOMEDULLIN.
FT PROPEP   148   188   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT DISULFID   110   115   BY SIMILARITY.
FT MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT CONFLICT   130   130   N -> K (IN REF. 2).
SQ SEQUENCE   188 AA; 20929 MW; 809D6A64F98F5578 CRC64;

Query Match   93.6%;   Score 265; DB 1; Length 188;
Best Local Similarity   94.2%;   Pred. No. 3.4e-28;
Matches   49; Conservative   0; Mismatches   0; Indels   3; Gaps   0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
           |||||||||||||||||||||||||||||||||| ||||| |||||||||||
Db   95 YRQSMNNFQGPRSFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146

RESULT 4
ADML_BOVIN
ID ADML_BOVIN   STANDARD;   PRT;   188 AA.
AC O62827;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98244567; PubMed=9585168;
RA Barker S., Wood E., Clark A.J.L., Corder R.;
RT "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT expression in vascular endothelial cells by staurosporine.";
RL Life Sci. 62:1407-1415(1998).
CC -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC   CIRCULATION CONTROL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; AJ001613; CAA04866.1; -.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL   1   21   BY SIMILARITY.
FT PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP   45   92   BY SIMILARITY.
FT PEPTIDE   95   146   ADRENOMEDULLIN.
FT PROPEP   148   188   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT DISULFID   110   115   BY SIMILARITY.
FT MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
SQ SEQUENCE   188 AA; 20981 MW; 3002E79A3B6612C CRC64;

Query Match   92.9%;   Score 263; DB 1; Length 188;
Best Local Similarity   92.3%;   Pred. No. 6.4e-28;
Matches   48; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
           |||| |||||||||||||||||||||||||| |||||||| |||||||||||
Db   95 YRQSLNNFQGLRSFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146

RESULT 5
ADML_RAT
ID ADML_RAT   STANDARD;   PRT;   185 AA.
AC P43145;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=9384621; PubMed=7690563;
RA Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA Matsuo H., Eto T.;
RT "Molecular cloning and biological activities of rat adrenomedullin, a
RT hypotensive peptide.";
RL Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96102137; PubMed=8524787;
RA Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT its role in exacerbating focal brain ischemic damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC   AGENTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC   HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC ---
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DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21   BY SIMILARITY.
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   91   BY SIMILARITY.
FT   PEPTIDE   94   143   ADRENOMEDULLIN.
FT   PROPEP   149   185   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   107   112   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   MOD_RES   143   143   AMIDATION (G-144 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
SQ   SEQUENCE   185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;

Query Match   81.6%;
Best Local Similarity   84.6%;   Score 231; DB 1; Length 185;
Matches   44; Conservative   3; Mismatches   3; Indels   2; Gaps   1;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
          ||||||| ||| |||||||||||||||||||||||| :||:|||||||
Db   94 YRQSMN-QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143

RESULT 6
ADML_MOUSE
ID   ADML_MOUSE   STANDARD;   PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RA   Yotsumoto S., Ko M.S.H.;
RT   "Expression of mouse adrenomedullin gene in trophoblastic giant
RT   cells at the implantation site.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC   AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   --

DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21   BY SIMILARITY.
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92   BY SIMILARITY.
FT   PEPTIDE   95   144   ADRENOMEDULLIN.
FT   PROPEP   151   184   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   108   113   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   MOD_RES   144   144   AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   CONFLICT   173   173   A -> G (IN REF. 2).
SQ   SEQUENCE   184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match   78.4%;
Best Local Similarity   82.7%;   Pred. No. 1.8e-22; Length 184;
Matches   43; Conservative   2; Mismatches   5; Indels   2; Gaps   1;

Qy   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
          ||||||| |||||||||||||||||||||||| :|||||||||||||
Db   95 YRQSMN-QGSRSNGCRFGTCTFQKLAHQIYQLTDKDKDGMAPRNKISPQGY 144

RESULT 7
TYRO_RANNI
ID   TYRO_RANNI   STANDARD;   PRT;   532 AA.
AC   Q04604;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
GN   TYR OR TYRS.
OS   Rana nigromaculata (Japanese pond frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93077054; PubMed=1446833;
RA   Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;
RT   "Analysis of the tyrosinase gene of the Japanese pond frog, Rana
RT   nigromaculata: cloning and sequencing of the cDNA encoding tyrosinase of the
RT   Japanese pond frog, Rana nigromaculata.";
RL   Jpn. J. Genet. 70:79-82(1995).
RN   [2]
RP   SEQUENCE OF 1-277 FROM N.A.
RC   TISSUE=blood;
RX   MEDLINE=95290234; PubMed=7772385;
RA   Miura I., Okumoto H., Makino K., Nakata A., Nishioka M.;
RT   "Analysis of the tyrosinase gene of the Japanese pond frog, Rana
RT   nigromaculata: cloning and nucleotide sequence of the genomic DNA
RT   containing the tyrosinase gene and its flanking regions.";
RL   Gene 121:359-363(1992).
CC   -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC   THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC   COMPOUNDS.
CC   -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC   DOPAquinone + H(2)O.
CC   -!- COFACTOR: BINDS TWO COPPER IONS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC   -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC   --

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CC   -------------------------------------------------------------------------
DR   EMBL; D12514; BAA02077.1; -.
DR   EMBL; D37779; BAA07034.1; -.
DR   PIR; JC1392; JC1392.
DR   InterPro; IPR002227; Tyrosinase.
DR   Pfam; PF00264; tyrosinase; 1.
DR   PRINTS; PR00092; TYROSINASE.
DR   PROSITE; PS00497; TYROSINASE_1; 1.
DR   PROSITE; PS00498; TYROSINASE_2; 1.
KW   Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
KW   Transmembrane; Melanin biosynthesis.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    532       TYROSINASE.
FT   DOMAIN       20    475       LUMENAL, MELANOSOME (POTENTIAL).
FT   TRANSMEM    476    499       POTENTIAL.
FT   DOMAIN      500    532       CYTOPLASMIC (POTENTIAL).
FT   METAL       184    184       COPPER A (BY SIMILARITY).
FT   METAL       206    206       COPPER A (BY SIMILARITY).
FT   METAL       215    215       COPPER A (BY SIMILARITY).
FT   METAL       367    367       COPPER B (BY SIMILARITY).
FT   METAL       371    371       COPPER B (BY SIMILARITY).
FT   METAL       394    394       COPPER B (BY SIMILARITY).
FT   CARBOHYD     90     90       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    115    115       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    375    375       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT      10     10       T -> A.
SQ   SEQUENCE   532 AA;  60115 MW;  B27D3080F0C74B3A CRC64;

Query Match             23.1%;  Score 65.5;  DB 1;  Length 532;
Best Local Similarity   33.9%;  Pred. No. 0.4;
Matches   20;  Conservative   8;  Mismatches   18;  Indels   13;  Gaps   4;

Qy   3 QSMNNFQGLRSFGCRFG----TCTVQK-LAHQIYQFTDKDKD------NVAPRSKISP 49
         |   |||||   ||||  : .  :|::: ::| .:  |:|    |||
Db  94 QCCQNFMGVNCGECRFGYTGPNCTVRRNMIRKDIFRMTAEKDKLIAYLNLA-KHTISP 151


RESULT 8
MRP2_RAT
ID   MRP2_RAT     STANDARD;      PRT;   1541 AA.
AC   Q63120; Q63145;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 2 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein).
GN   ABCC2 OR CMOAT OR MRP2 OR CMRP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=96180672; PubMed=8599091;
RA   Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M.,
RA   Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
RT   "Congenital jaundice in rats with a mutation in a multidrug
RT   resistance-associated protein gene.";
RL   Science 271:1126-1128(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=96279006; PubMed=8662992;
RA   Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
RA   Keppler D.;
RT   "cDNA cloning of the hepatocyte canalicular isoform of the multidrug
RT   resistance protein, cMrp, reveals a novel conjugate export pump
RT   deficient in hyperbilirubinemic mutant rats.";
RL   J. Biol. Chem. 271:15091-15098(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA   Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Sugiyama Y.;
RT   "Expression of the putative ATP-binding cassette region, homologous to
RT   that in multidrug resistance associated protein (MRP), is hereditarily
RT   defective in Eisai hyperbilirubinemic rats (EHBR).";
RL   Int. Hepatol. Commun. 292:292-299(1996)
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC       ANIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
CC   -!- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED
CC       HYPERBILIRUBINEMIA (EHBR).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; L49379; AAC42087.1; -.
DR   EMBL; X96393; CAA65257.1; -.
DR   EMBL; D86086; BAA13016.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT   DOMAIN        1     26       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     27     47       1 (BY SIMILARITY).
FT   DOMAIN       48     67       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     68     88       2 (BY SIMILARITY).
FT   DOMAIN       89     92       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     93    113       3 (BY SIMILARITY).
FT   DOMAIN      114    125       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    126    146       4 (BY SIMILARITY).
FT   DOMAIN      147    164       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    165    185       5 (BY SIMILARITY).
FT   DOMAIN      186    309       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    310    330       6 (BY SIMILARITY).
FT   DOMAIN      331    356       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    357    377       7 (BY SIMILARITY).
FT   DOMAIN      378    433       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    434    454       8 (BY SIMILARITY).
FT   DOMAIN      455    457       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    458    478       9 (BY SIMILARITY).
FT   DOMAIN      479    540       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    541    561       10 (BY SIMILARITY).
FT   DOMAIN      562    583       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    584    604       11 (BY SIMILARITY).
FT   DOMAIN      605    967       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    968    988       12 (BY SIMILARITY).
FT   DOMAIN      989   1029       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1030   1050       13 (BY SIMILARITY).
FT   DOMAIN     1051   1093       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1094   1114       14 (BY SIMILARITY).
FT   DOMAIN     1115   1115       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1116   1136       15 (BY SIMILARITY).
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FT   DOMAIN     1137   1207   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1208   1228   16 (BY SIMILARITY).
FT   DOMAIN     1229   1230   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1231   1251   17 (BY SIMILARITY).
FT   DOMAIN     1252   1541   CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND     667    674   ATP (POTENTIAL).
FT   NP_BIND    1330   1337   ATP (POTENTIAL).
FT   CARBOHYD      6      6   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1007   1007   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1010   1010   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1011   1011   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    420    420   M -> V (IN REF. 3).
FT   SEQUENCE   1541 AA:  173383 MW;  D5FB55571BFDDB39 CRC64;

Query Match             21.6%;  Score 61;  DB 1;  Length 1541;
Best Local Similarity   38.2%;  Pred. No. 4.8;
Matches   13;  Conservative    4;  Mismatches   17;  Indels    0;  Gaps     0;

Qy    18  FSQCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG   51
Db  1479  FSQCTVTTIAHRLHTIMDSDKIMVLDNGKIVEYG  1512


RESULT 9
TYRO_COTJA
ID   TYRO_COTJA     STANDARD;      PRT;   273 AA.
AC   Q08410;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
DE   (Fragment).
GN   TYR.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93181407; PubMed=1292011;
RA   Yamamoto H., Kudo T., Masuko N., Miura H., Sato S., Tanaka M.,
RA   Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;
RT   "Phylogeny of regulatory regions of vertebrate tyrosinase genes.";
RL   Pigment Cell Res. 5:284-294(1992).
CC   -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC       THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC       COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
CC       DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
CC       INDOLE-5,6 QUINONE.
CC   -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC       DOPAquinone + H(2)O.
CC   -!- COFACTOR: BINDS TWO COPPER IONS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC   -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC   --------------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; S56788; AAB25510.1; -.
DR   InterPro; IPR002227; Tyrosinase.
DR   Pfam; PF00264; tyrosinase; 1.
DR   PROSITE; PS00497; TYROSINASE_1; 1.
DR   PROSITE; PS00498; TYROSINASE_2; PARTIAL.
KW   Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
KW   Transmembrane; Melanin biosynthesis.
FT   SIGNAL        1     18   POTENTIAL.
FT   CHAIN        19   >273   TYROSINASE.
```

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FT   METAL       180    180   COPPER A (BY SIMILARITY).
FT   METAL       202    202   COPPER A (BY SIMILARITY).
FT   METAL       211    211   COPPER A (BY SIMILARITY).
FT   CARBOHYD     86     86   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    111    111   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     273    273
FT   SEQUENCE    273 AA;  31499 MW;  0EA3DE55BE1EA1A CRC64;

Query Match             20.8%;  Score 59;  DB 1;  Length 273;
Best Local Similarity   35.9%;  Pred. No. 1.5;
Matches   14;  Conservative    6;  Mismatches   13;  Indels   6;  Gaps     2;

Qy     7  NFQGLRSFGCRFG---TCTVQKL--AHQIYQFTDKDKD   39
Db    94  NFMGFNCGECKFGFSGQNCTERRLRTRRNIFQLTIREKD  132


RESULT 10
MRP2_HUMAN
ID   MRP2_HUMAN     STANDARD;      PRT;   1545 AA.
AC   Q92887; Q99663; Q92798; Q14022; Q92500; Q90MS2;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 1 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein).
GN   ABCC2 OR CMOAT1 OR CMOAT OR MRP2 OR CMRP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96390592; PubMed=8797578;
RA   Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M.,
RA   Kagotani K., Okumura K., Akiyama S., Kuwano M.;
RT   "A human canalicular multispecific organic anion transporter (cMOAT)
RT   gene is overexpressed in cisplatin-resistant human cancer cell lines
RT   with decreased drug accumulation.";
RL   Cancer Res. 56:4124-4129(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
RA   Baas F., Borst P.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96279006; PubMed=8662992;
RA   Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
RA   Keppler D.;
RT   "cDNA cloning of the hepatocyte canalicular isoform of the multidrug
RT   resistance protein, cMrp, reveals a novel conjugate export pump
RT   deficient in hyperbilirubinemic mutant rats.";
RL   J. Biol. Chem. 271:15091-15098(1996).
RN   [4]
RP   REVISIONS.
RA   Keppler D.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99395001; PubMed=10464142;
RA   Tsujii H., Koenig J., Rost D., Stoeckel B., Leuschner U., Keppler D.;
RT   "Exon-intron organization of the human multidrug-resistance protein 2
RT   (MRP2) gene mutated in Dubin-Johnson syndrome.";
RL   Gastroenterology 117:653-660(1999).
RN   [6]
RP   VARIANT DJS TRP-768.
RX   MEDLINE=98087571; PubMed=9425227;
RA   Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
RA   Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
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RT   "Mutations in the canilicular multispecific organic anion transporter
RT   (cMOAT) gene, a novel ABC transporter, in patients with
RT   hyperbilirubinemia II/Dubin-Johnson syndrome.";
RL   Hum. Mol. Genet. 7:203-207(1998).
RN   [7]
RP   VARIANTS DJS TRP-768 AND ARG-1382.
RX   MEDLINE=99162196; PubMed=10053008;
RA   Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y.,
RA   Adachi Y., Sakisaka S., Kuwano M.;
RT   "Genomic structure of the canalicular multispecific organic anion-
RT   transporter gene (MRP2/cMOAT) and mutations in the ATP-binding-
RT   cassette region in Dubin-Johnson syndrome.";
RL   Am. J. Hum. Genet. 64:739-746(1999).
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC       ANIONS. MAY FUNCTION AS A CELLULAR CISPLATIN TRANSPORTER.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
CC   -!- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF DUBIN-JOHNSON SYNDROME
CC       (DJS), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONJUGATED
CC       HYPERBILIRUBINEMIA, AN INCREASE IN THE URINARY EXCRETION OF
CC       COPROPORPHYRIN ISOMER I, DEPOSITION OF MELANIN-LIKE PIGMENT IN
CC       HEPATOCYTES, AND PROLONGED RETENTION OF SULFOBROMOPHTHALEIN, BUT
CC       OTHERWISE NORMAL LIVER FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U63970; AAB39892.1; -.
DR   EMBL; U49248; AAB09422.1; -.
DR   EMBL; X96395; CAA65259.2; -.
DR   EMBL; AJ132244; CAB45309.1; -.
DR   EMBL; AJ132287; CAB45309.1; JOINED.
DR   EMBL; AJ245625; CAB45309.1; JOINED.
DR   EMBL; AJ132288; CAB45309.1; JOINED.
DR   EMBL; AJ132289; CAB45309.1; JOINED.
DR   EMBL; AJ132290; CAB45309.1; JOINED.
DR   EMBL; AJ132291; CAB45309.1; JOINED.
DR   EMBL; AJ132292; CAB45309.1; JOINED.
DR   EMBL; AJ132293; CAB45309.1; JOINED.
DR   EMBL; AJ132294; CAB45309.1; JOINED.
DR   EMBL; AJ132295; CAB45309.1; JOINED.
DR   EMBL; AJ132296; CAB45309.1; JOINED.
DR   EMBL; AJ132297; CAB45309.1; JOINED.
DR   EMBL; AJ132298; CAB45309.1; JOINED.
DR   EMBL; AJ132299; CAB45309.1; JOINED.
DR   EMBL; AJ132300; CAB45309.1; JOINED.
DR   EMBL; AJ132301; CAB45309.1; JOINED.
DR   EMBL; AJ132302; CAB45309.1; JOINED.
DR   EMBL; AJ132303; CAB45309.1; JOINED.
DR   EMBL; AJ245626; CAB45309.1; JOINED.
DR   EMBL; AJ132304; CAB45309.1; JOINED.
DR   EMBL; AJ132305; CAB45309.1; JOINED.
DR   EMBL; AJ132306; CAB45309.1; JOINED.
DR   EMBL; AJ132308; CAB45309.1; JOINED.
DR   EMBL; AJ245627; CAB45309.1; JOINED.
DR   EMBL; AJ132309; CAB45309.1; JOINED.
DR   EMBL; AJ132310; CAB45309.1; JOINED.
DR   EMBL; AJ132311; CAB45309.1; JOINED.
DR   EMBL; AJ132312; CAB45309.1; JOINED.
DR   EMBL; AJ132313; CAB45309.1; JOINED.
DR   EMBL; AJ132314; CAB45309.1; JOINED.
DR   HSSP; P13569; 1NBD.
DR   MIM; 601107; -.
DR   MIM; 237500; -.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transport.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
KW   Disease mutation.
FT   DOMAIN        1     27   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     28     48   1 (BY SIMILARITY).
FT   DOMAIN       49     68   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     69     89   2 (BY SIMILARITY).
FT   DOMAIN       90     93   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     94    114   3 (BY SIMILARITY).
FT   DOMAIN      115    126   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    127    147   4 (BY SIMILARITY).
FT   DOMAIN      148    165   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    166    186   5 (BY SIMILARITY).
FT   DOMAIN      187    313   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    314    334   6 (BY SIMILARITY).
FT   DOMAIN      335    360   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    361    381   7 (BY SIMILARITY).
FT   DOMAIN      382    437   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN      438    458   8 (BY SIMILARITY).
FT   TRANSMEM    459    461   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN      462    482   9 (BY SIMILARITY).
FT   TRANSMEM    483    544   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN      545    565   10 (BY SIMILARITY).
FT   TRANSMEM    566    587   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN      588    608   11 (BY SIMILARITY).
FT   TRANSMEM    609    971   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN      972    992   12 (BY SIMILARITY).
FT   TRANSMEM    993   1033   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN     1034   1054   13 (BY SIMILARITY).
FT   TRANSMEM   1055   1097   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN     1098   1118   14 (BY SIMILARITY).
FT   TRANSMEM   1119   1119   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN     1120   1140   15 (BY SIMILARITY).
FT   TRANSMEM   1141   1211   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN     1212   1232   16 (BY SIMILARITY).
FT   TRANSMEM   1233   1234   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN     1235   1255   17 (BY SIMILARITY).
FT   TRANSMEM   1256   1545   CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND     671    678   ATP (POTENTIAL).
FT   NP_BIND    1334   1341   ATP (POTENTIAL).
FT   CARBOHYD      7      7   N-LINKED (GLCNAC...   .) (POTENTIAL).
FT   CARBOHYD     12     12   N-LINKED (GLCNAC...   .) (POTENTIAL).
FT   CARBOHYD   1011   1011   N-LINKED (GLCNAC...   .) (POTENTIAL).
FT   VARIANT     768    768   R -> W (IN DJS).
FT                           /FTId=VAR_000099.
FT   VARIANT    1382   1382   Q -> R (IN DJS).
FT                           /FTId=VAR_010756.
FT   CONFLICT   1188   1188   V -> E (IN REF. 2).
FT   CONFLICT   1430   1430   V -> G (IN REF. 5).
FT   CONFLICT   1515   1515   C -> Y (IN REF. 2).
SQ   SEQUENCE   1545 AA;  174190 MW;  EA1266A4DDF391 CRC64;

Query Match             20.8%;  Score 59;  DB 1;  Length 1545;
Best Local Similarity   37.8%;  Pred. No. 8.9;
Matches   14;  Conservative    5;  Mismatches   14;  Indels   14;  Gaps    4;

Qy     18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 50
          | ||| :||::||: ||:|::::   ||  ||
Db   1483 FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSGPE 1519

RESULT 11
TYRO_CHICK
ID   TYRO_CHICK     STANDARD;      PRT;    529 AA.
AC   P55024;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
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DE   Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
GN   TYR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WHITE LEGHORN;
RX   MEDLINE=93157254; PubMed=1494538;
RA   Mochii M., Iio A., Yamamoto H., Takeuchi T., Eguchi G.;
RT   "Isolation and characterization of a chicken tyrosinase cDNA.";
RL   Pigment Cell Res. 5:162-167(1992).
RN   [2]
RP   SEQUENCE OF 1-273 FROM N.A.
RX   MEDLINE=96194800; PubMed=8647445;
RA   Ferguson C.A., Kidson S.H.;
RT   "Characteristic sequences in the promoter region of the chicken
RT   tyrosinase-encoding gene.";
RL   Gene 169:191-195(1996).
CC   -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC       THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC       COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
CC       DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
CC       INDOLE-5,6 QUINONE.
CC   -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC       DOPAquinone + H(2)O.
CC   -!- COFACTOR: BINDS TWO COPPER IONS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC   -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; D88349; BAA13590.1; -.
DR   EMBL; L46805; AAB08441.1; -.
DR   InterPro; IPR002227; Tyrosinase.
DR   Pfam; PF00264; tyrosinase; 1.
DR   PRINTS; PR00092; TYROSINASE.
DR   PROSITE; PS00497; TYROSINASE_1; 1.
DR   PROSITE; PS00498; TYROSINASE_2; 1.
KW   Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
KW   Transmembrane; Melanin biosynthesis.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    529       TYROSINASE.
FT   DOMAIN       19    476       LUMENAL, MELANOSOME (POTENTIAL).
FT   TRANSMEM    477    497       POTENTIAL.
FT   DOMAIN      498    529       CYTOPLASMIC (POTENTIAL).
FT   METAL       180    180       COPPER A (BY SIMILARITY).
FT   METAL       202    202       COPPER A (BY SIMILARITY).
FT   METAL       211    211       COPPER A (BY SIMILARITY).
FT   METAL       363    363       COPPER B (BY SIMILARITY).
FT   METAL       367    367       COPPER B (BY SIMILARITY).
FT   METAL       390    390       COPPER B (BY SIMILARITY).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    290    290       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. .  .) (POTENTIAL).
FT   CARBOHYD    371    371       N-LINKED (GLCNAC. .  .) (POTENTIAL).
SQ   SEQUENCE   529 AA;  60357 MW;  74B464A52C3EFBF5 CRC64;

Query Match             20.1%;  Score 57;  DB 1;  Length 529;
Best Local Similarity   35.9%;  Pred. No. 5.4;
Matches   14;  Conservative    5;  Mismatches   14;  Indels    6;  Gaps    2;

Qy    7  NFQGLRSFGCRFG---TCTVQKL--AHQIYQFTDKDKD  39
         ||  ||   |  :||        || :||    :| ||  :||
Db   94  NFMGFNCGECKFGFSGQNCTERRLRTRRNIFQLTISEKD  132


RESULT 12
SYH_METTH
ID   SYH_METTH     STANDARD;      PRT;    425 AA.
AC   O26346;
DT   15-JUL-1998 (Rel. 36, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE   (HisRS).
GN   HISS OR MTH244.
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC       diphosphate + L-histidyl-tRNA(His).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; AE000811; AAB84750.1; ALT_INIT.
DR   HSSP; O32422; 1QE0.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   InterPro; IPR004154; HGTP_anticodon.
DR   InterPro; IPR002314; tRNA-synt_2b.
DR   Pfam; PF03129; HGTP_anticodon; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
SQ   SEQUENCE   425 AA;  48019 MW;  8388A5975A017535 CRC64;

Query Match             19.4%;  Score 55;  DB 1;  Length 425;
Best Local Similarity   31.7%;  Pred. No. 8;
Matches   13;  Conservative   11;  Mismatches   13;  Indels    4;  Gaps    1;

Qy    8  FOGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKIS  48
         |:|:| |         :||:|||||||||||||  :|  |::
Db   44  FEELKLFTVKSG---EEVVNQIYHFTDKGGRELALRPELT  80


RESULT 13
MRP2_RABIT
ID   MRP2_RABIT    STANDARD;      PRT;   1564 AA.
AC   Q28689;
```

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DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 1 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein) (Epithelial basolateral chloride conductance regulator).
GN   ABCC2 OR MRP2 OR EBCR.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ileum;
RX   MEDLINE=96224297; PubMed=8643587;
RA   van Kuijck M.A., van Aubel R.A.M.H., Busch A.E., Lang F.,
RA   Russel F.G.M., Bindels R.J.M., van Os C.H., Deen P.M.T.;
RT   "Molecular cloning and expression of a cyclic AMP-activated chloride
RT   conductance regulator: a novel ATP-binding cassette transporter.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=98279125; PubMed=9614209;
RA   van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
RA   van Os C.H., Russel F.G.M.;
RT   "Adenosine triphosphate-dependent transport of anionic conjugates by
RT   the rabbit multidrug resistance-associated protein Mrp2 expressed in
RT   insect cells.";
RL   Mol. Pharmacol. 53:1062-1067(1998).
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC       ANIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SMALL
CC       INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
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DR   EMBL; Z49144; CAA89004.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT   DOMAIN        1     27       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     28     48       1 (BY SIMILARITY).
FT   DOMAIN       49     68       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     69     89       2 (BY SIMILARITY).
FT   DOMAIN       90     93       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     94    114       3 (BY SIMILARITY).
FT   DOMAIN      115    126       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    127    147       4 (BY SIMILARITY).
FT   DOMAIN      148    165       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    166    186       5 (BY SIMILARITY).
FT   DOMAIN      187    311       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    312    332       6 (BY SIMILARITY).
FT   DOMAIN      333    358       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    359    379       7 (BY SIMILARITY).
FT   DOMAIN      380    435       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    436    456       8 (BY SIMILARITY).
FT   DOMAIN      457    459       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    460    480       9 (BY SIMILARITY).
FT   DOMAIN      481    542       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    543    563       10 (BY SIMILARITY).
FT   DOMAIN      564    585       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    586    606       11 (BY SIMILARITY).
FT   DOMAIN      607    969       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    970    990       12 (BY SIMILARITY).
FT   DOMAIN      991   1031       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1032   1052       13 (BY SIMILARITY).
FT   DOMAIN     1053   1095       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1096   1116       14 (BY SIMILARITY).
FT   DOMAIN     1117   1117       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1118   1138       15 (BY SIMILARITY).
FT   DOMAIN     1139   1209       CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1210   1230       16 (BY SIMILARITY).
FT   DOMAIN     1231   1232       EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1233   1253       17 (BY SIMILARITY).
FT   DOMAIN     1254   1543       CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND     669    676       ATP (POTENTIAL).
FT   NP_BIND    1332   1339       ATP (POTENTIAL).
FT   CARBOHYD      7      7       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     12     12       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   1009   1009       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   1564 AA;  175542 MW;  D8FBF5AC8FE45873 CRC64;

Query Match             19.4%;  Score 55;  DB 1;  Length 1564;
Best Local Similarity   35.3%;  Pred. No. 31;
Matches   12;  Conservative   4;  Mismatches   18;  Indels   0;  Gaps   0;

Qy       18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 51
            |  ||| :|||:::|    || |   | |    |
Db     1481 FSHCTVITIAHRLHTIMDSDKIMVLDNGNIVEYG 1514

RESULT 14
SLS6_BRAOL
ID   SLS6_BRAOL     STANDARD;      PRT;     436 AA.
AC   P07761;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   S-locus-specific glycoprotein S6 precursor (SLSG-6).
GN   SLSG.
OS   Brassica oleracea (Cauliflower).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3712;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
RT   "Amino-acid sequence of glycoproteins encoded by three alleles of the
RT   s locus of Brassica oleracea.";
RL   Nature 326:617-619(1987).
RN   [2]
RP   SEQUENCE OF 22-435 FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RT   "A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
RT   oleracea.";
RL   Nature 318:263-267(1985).
RN   [3]
RP   ERRATUM.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RL   Nature 326:523-523(1987).
CC   -!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC       (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
CC   -!- TISSUE SPECIFICITY: STIGMA.
CC   -!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
CC       B.OLERACEA.
CC   -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
CC       KINASE RECEPTOR (ZMPK1).
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CC    use by non-profit institutions as long as its content is in no way
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    -----------------------------------------------------------------------
DR    EMBL; Y00268; CAA68375.1; -.
DR    EMBL; X03170; CAA26934.1; ALT_INIT.
DR    PIR; A27827; A27827.
DR    InterPro; IPR001480; B_lectin.
DR    InterPro; IPR003609; Pan_app.
DR    InterPro; IPR000858; Slocus_glycop.
DR    Pfam; PF01453; Agglutinin; 1.
DR    Pfam; PF00954; S_locus_glycop; 1.
DR    SMART; SM00108; B_lectin; 1.
DR    SMART; SM00473; PAN_AP; 1.
KW    Self-incompatibility; Glycoprotein; Polymorphism; Signal.
FT    SIGNAL        1     31       POTENTIAL.
FT    CHAIN        32    436       S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
FT    CARBOHYD     46     46       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD     64     64       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    114    114       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    121    121       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    245    245       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    261    261       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    390    390       N-LINKED (GLCNAC...)  (POTENTIAL).
SQ    SEQUENCE   436 AA;  49779 MW;  E2332635B885A515 CRC64;

Query Match             19.3%;  Score  54.5;  DB 1;  Length 436;
Best Local Similarity   28.6%;
Matches   14;  Conservative  10;  Mismatches  14;  Indels  11;  Gaps   2;

Qy    15  GCRF-GTCTVQKLAHQIYQFTDKDKD--------NVAPRSKISPQGY 52
              ||| ||||::: |:|||:. ::         :|:|:||
Db   227  GVRFSGIPEDQKLSMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275


RESULT 15
TYRO_HUMAN
ID   TYRO_HUMAN    STANDARD;    PRT;    529 AA.
AC   P14679; Q15676; Q15675; Q15680;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
DE   (Tumor rejection antigen AB) (SK29-AB) (LB24-AB).
GN   TYR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91236163; PubMed=1903356;
RA   Giebel L.B., Strunk K.M., Spritz R.A.;
RT   "Organization and nucleotide sequences of the human tyrosinase gene
RT   and a truncated tyrosinase-related segment.";
RL   Genomics 9:435-445(1991).
RN   [2]
RP   REVISIONS TO 384-398.
RX   MEDLINE=88041128; PubMed=2823263;
RA   Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;
RT   "Isolation and sequence of a cDNA clone for human tyrosinase that
RT   maps at the mouse c-albino locus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:6352-6352(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Melanoma;
RX   MEDLINE=89279151; PubMed=2499655;
RA   Bouchard B., Fuller B.B., Vijayasaradhi S., Houghton A.N.;
RT   "Induction of pigmentation in mouse fibroblasts by expression of
RT   human tyrosinase cDNA.";
RL   J. Exp. Med. 169:2029-2042(1989).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91271371; PubMed=1711223;
RA   Chintamaneni C.D., Halaban R., Kobayashi Y., Witkop C.J., Kwon B.S.;
RT   "A single base insertion in the putative transmembrane domain of the
RT   tyrosinase gene as a cause for tyrosinase-negative oculocutaneous
RT   albinism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5272-5276(1991).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Melanoma, and T-cell;
RX   MEDLINE=93340625; PubMed=840755;
RA   Brichard V., van Pel A., Woelfel T., Woelfel C., de Plaen E.,
RA   Lethe B., Coulie P., Boon T.;
RT   "The tyrosinase gene codes for an antigen recognized by autologous
RT   cytolytic T lymphocytes on HLA-A2 melanomas.";
RL   J. Exp. Med. 178:489-495(1993).
RN   [7]
RP   SEQUENCE OF 1-272 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=90089403; PubMed=2480811;
RA   Kikuchi H., Miura H., Yamamoto H., Takeuchi T., Del T., Watanabe M.;
RT   "Characteristic sequences in the upstream region of the human
RT   tyrosinase gene.";
RL   Biochim. Biophys. Acta 1009:283-286(1989).
RN   [8]
RP   SEQUENCE OF 1-32 FROM N.A.
RX   MEDLINE=89351001; PubMed=2504160;
RA   Takeda A., Tomita Y., Okinaga S., Tagami H., Shibahara S.;
RT   "Functional analysis of the cDNA encoding human tyrosinase
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 162:984-990(1989).
RN   [9]
RP   REVIEW ON OCA VARIANTS.
RX   MEDLINE=93237884; PubMed=8477259;
RA   Oetting W.S., King R.A.;
RT   "Molecular basis of type I (tyrosinase-related) oculocutaneous
RT   albinism: mutations and polymorphisms of the human tyrosinase gene.";
RL   Hum. Mutat. 2:1-6(1993).
RN   [10]
RP   REVIEW ON OCA-I VARIANTS.
RX   MEDLINE=99140254; PubMed=10094567;
RA   Oetting W.S., King R.A.;
RT   "Molecular basis of albinism: mutations and polymorphisms of
RT   pigmentation genes associated with albinism.";
RL   Hum. Mutat. 13:99-115(1999).
RN   [11]
RP   VARIANTS TYR-192; GLN-402; OCA-IA LYS-373 AND OCA-IA ASN-383.
RX   MEDLINE=90259036; PubMed=2342539;
RA   Spritz R.A., Strunk K.M., Giebel L.B., King R.A.;
RT   "Detection of mutations in the tyrosinase gene in a patient with type
RT   IA oculocutaneous albinism.";
RL   New Engl. J. Med. 322:1724-1728(1990).
RN   [12]
RP   VARIANT OCA-IA LEU-81.
RX   MEDLINE=90238992; PubMed=1970634;
RA   Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;
RT   "A frequent tyrosinase gene mutation in classic, tyrosinase-negative
RT   (type IA) oculocutaneous albinism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258(1990).
RN   [13]
RP   VARIANTS OCA-IB PHE-275 AND LEU-406.
RX   MEDLINE=91241133; PubMed=1903591;
RA   Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,
RA   King R.A., Spritz R.A.;
RT   "Tyrosinase gene mutations associated with type IB ('yellow')
RT   oculocutaneous albinism.";
RL   Am. J. Hum. Genet. 48:1159-1167(1991).
RN   [14]
```

RP ERRATUM.
RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,
RA King R.A., Spritz R.A.;
RL Am. J. Hum. Genet. 49:696-696(1991).
RN [15]
RP VARIANTS OCA-IA SER-21; TRP-217; HIS-299; SER-403; SER-446 AND
RP ASN-448.
RX MEDLINE=92351982; PubMed=1642278;
RA Tripathi R.K., Strunk K.M., Giebel L.B., Weleber R.G., Spritz R.A.;
RT "Tyrosinase gene mutations in type I (tyrosinase-deficient)
RT oculocutaneous albinism define two clusters of missense
RT substitutions.";
RL Am. J. Med. Genet. 43:865-871(1992).
RN [16]
RP VARIANT OCA-IA ARG-89.
RX MEDLINE=91118940; PubMed=1899321;
RA Spritz R.A., Strunk K.M., Hsieh C.-L., Sekhon G.S., Francke U.;
RT "Homozygous tyrosinase gene mutation in an American black with
RT tyrosinase-negative (type IA) oculocutaneous albinism.";
RL Am. J. Hum. Genet. 48:318-324(1991).
RN [17]
RP VARIANT OCA-ITS GLN-422.
RX MEDLINE=91154384; PubMed=1900309;
RA Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;
RT "A tyrosinase gene missense mutation in temperature-sensitive type I
RT oculocutaneous albinism. A human homologue to the Siamese cat and the
RT Himalayan mouse.";
RL J. Clin. Invest. 87:1119-1122(1991).
RN [18]
RP VARIANTS OCA-IA GLY-42; TYR-55; THR-206 AND ARG-419.
RX MEDLINE=92048465; PubMed=1943686;
RA King R.A., Mentink M.M., Oetting W.S.;
RT "Non-random distribution of missense mutations within the human
RT tyrosinase gene in type I (tyrosinase-related) oculocutaneous
RT albinism.";
RL Mol. Biol. Med. 8:19-29(1991).
RN [19]
RP VARIANTS OCA-IA ILE-176 AND GLN-217.
RX MEDLINE=93138611; PubMed=1487241;
RA Oetting W.S., King R.A.;
RT "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous
RT albinism.";
RL Hum. Genet. 90:258-262(1992).
RN [20]
RP VARIANTS OCA-IA GLN-328; ARG-419 AND LEU-431.
RX MEDLINE=94070862; PubMed=7902671;
RA Tripathi R.K., Bundey S., Musarella M.A., Droetto S., Strunk K.M.,
RA Holmes S.A., Spritz R.A.;
RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type
RT I (tyrosinase-deficient) oculocutaneous albinism (OCA).";
RL Am. J. Hum. Genet. 53:1173-1179(1993).
RN [21]
RP VARIANTS OCA-IA D-47; C-217 DEL; H-299 AND LYS-373, AND VARIANTS OCA-IB
RP S-152 AND K-294.
RX MEDLINE=94175072; PubMed=8128955;
RA Gershoni-Baruch R., Rosenmann A., Droetto S., Holmes S.,
RA Tripathi R.K., Spritz R.A.;
RT "Mutations of the tyrosinase gene in patients with oculocutaneous
RT albinism from various ethnic groups in Israel.";
RL Am. J. Hum. Genet. 54:586-594(1994).
RN [22]
RP VARIANTS OCA TYR-367; THR-370 AND LYS-373, AND VARIANT GLN-402.
RX MEDLINE=95043421; PubMed=7955413;
RA Breimer L.H., Winder A.F., Jay B., Jay M.;
RT "Initiation codon mutation of the tyrosinase gene as a cause of human
RT albinism.";
RL Clin. Chim. Acta 227:17-22(1994).
RN [23]
RP VARIANTS OCA-IA ARG-361 AND TYR-371.
RX MEDLINE=96243675; PubMed=8644824;
RA Summers C.G., Oetting W.S., King R.A.;
RT "Diagnosis of oculocutaneous albinism with molecular analysis.";
RL Am. J. Ophthalmol. 121:724-726(1996).

RN [24]
RP VARIANT GLN-402.
RX MEDLINE=97301760; PubMed=9158138;
RA Morell R., Spritz R.A., Ho L., Pierpont J., Guo W., Friedman T.B.,
RA Asher J.H. Jr.;
RT "Apparent digenic inheritance of Waardenburg syndrome type 2 (WS2) and
RT autosomal recessive ocular albinism (AROA).";
RL Hum. Mol. Genet. 6:659-664(1997).
RN [25]
RP VARIANTS OCA-IA AND OCA-IB.
RX MEDLINE=97403941; PubMed=9259202;
RA Spritz R.A., Oh J., Fukai K., Holmes S.A., Ho L., Chitayat D.,
RA France T.D., Musarella M.A., Orlow S.J., Schnur R.E., Weleber R.G.,
RA Levin A.V.;
RT "Novel mutations of the tyrosinase (TYR) gene in type I
RT oculocutaneous albinism (OCA).";
RL Hum. Mutat. 10:171-174(1997).
RN [26]
RP VARIANTS OCA-IA AND OCA-IB.
RA Oetting W.S., Fryer J.P., King R.A.;

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Query Match             18.7%;  Score 53;  DB 1;  Length 529;
Best Local Similarity   30.2%;  Pred. No. 19;
Matches  13;  Conservative  6;  Mismatches  6;  Indels  18;  Gaps  2;

Qy    3 QSMNNFQGLRSFGCRFG---TCTVQKL--AHQIYQFTDKDKD 39
          | ||| |:|   |:||    || ::|   |: ||:||
Db   90 QCSGNFMGFNCGNCKFGFWGPNCTERRLLVRRNIFDLSAPEKD 132
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Search completed: October 17, 2002, 14:49:13
Job time : 4.11222 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 9.48534 Seconds
         (without alignments)
         742.931 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence: 1 VSVALMVLGSLAFLGADTAR.........SKPQAHGAPAPPSGSAPHFL 182

Scoring table: BLOSUM62
         Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
         Maximum Match 100%
         Listing first 45 summaries

Database :   SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	947	100.0	185	1	ADML_HUMAN	P35318 homo sapien
2	817	86.3	188	1	ADML_PIG	P53366 sus scrofa
3	774.5	81.8	188	1	ADML_BOVIN	O62827 bos taurus
4	771	81.4	188	1	ADML_CANFA	O77559 canis famil
5	624.5	65.9	185	1	ADML_RAT	P43145 rattus norv
6	570	60.2	184	1	ADML_MOUSE	P97297 mus musculu
7	89.5	9.5	326	1	TTP_HUMAN	P26651 homo sapien
8	89	9.4	2224	1	FA5_HUMAN	P12259 homo sapien
9	88.5	9.3	397	1	CEFD_STRCL	P18549 streptomyce
10	87	9.2	450	1	A2AA_MOUSE	Q01338 mus musculu
11	87	9.2	656	1	DNAA_STRCO	P27902 streptomyce
12	83.5	8.8	574	1	MPI2_RAT	P48966 rattus norv
13	82	8.7	450	1	A2AA_RAT	P22909 rattus norv
14	80.5	8.5	682	1	TBR1_HUMAN	Q16650 homo sapien
15	80	8.4	250	1	REPA_AGRTU	P15394 agrobacteri
16	80	8.4	458	1	YNE1_CAEEL	P30640 caenorhabdi
17	79	8.3	320	1	TTP_RAT	P47973 rattus norv
18	79	8.3	450	1	A2AA_HUMAN	P08913 homo sapien
19	78.5	8.3	481	1	KR1_HSV2H	P13287 herpes simp
20	78.5	8.3	589	1	VP40_SCMVC	P16046 simian cyto
21	78.5	8.3	1796	1	YRF1_YEAST	P24088 saccharomyc
22	78.5	8.3	2145	1	CYAA_PODAN	Q01513 podospora a
23	78	8.2	519	1	GAG_SIVAT	P05892 simian immu
24	78	8.2	678	1	T2D5_MOUSE	Q62311 mus musculu
25	77.5	8.2	1382	1	YRF4_YEAST	O13559 saccharomyc
26	77.5	8.2	1681	1	YRF2_YEAST	P40105 saccharomyc
27	77.5	8.2	1859	1	YRF3_YEAST	P53345 saccharomyc
28	77.5	8.2	1859	1	YRF6_YEAST	P53819 saccharomyc
29	77	8.1	591	1	PTRR_MOUSE	P41593 mus musculu
30	77	8.1	678	1	T2D5_RAT	Q63801 rattus norv
31	76.5	8.1	450	1	A2AA_PIG	P18871 sus scrofa
32	76.5	8.1	681	1	TBR1_MOUSE	Q64336 mus musculu
33	76	8.0	410	1	ICP0_PRVIF	P29129 pseudorabie
34	75.5	8.0	2845	1	APC_MOUSE	Q61315 mus musculu
35	75	7.9	319	1	TTP_MOUSE	P22893 mus musculu
36	75	7.9	429	1	ELK1_MOUSE	P41969 mus musculu
37	75	7.9	591	1	PTRR_RAT	P25961 rattus norv
38	75	7.9	825	1	ICP0_HSV2H	P28284 herpes simp
39	75	7.9	1089	1	IMB3_YEAST	P32337 saccharomyc
40	74.5	7.9	127	1	CAL2_HUMAN	P10092 homo sapien
41	74.5	7.9	324	1	TTP_BOVIN	P53781 bos taurus
42	74.5	7.9	389	1	CBX8_HUMAN	Q9hc52 homo sapien
43	74.5	7.9	933	1	PRGR_HUMAN	P06401 homo sapien
44	74	7.8	423	1	BRAC_BRARE	Q07998 brachydanio
45	74	7.8	2254	1	CCAG_RAT	O54898 rattus norv

ALIGNMENTS

RESULT 1
ADML_HUMAN
ID   ADML_HUMAN   STANDARD;   PRT;   185 AA.
AC   P35318;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93343928; PubMed=7688224;
RA   Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT   "Cloning and characterization of cDNA encoding a precursor for human
RT   adrenomedullin.";
RL   Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94354869; PubMed=8074714;
RA   Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA   Kitamura K., Eto T., Matsuo H.;
RT   "Genomic structure of human adrenomedullin gene.";
RL   Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN   [3]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [4]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445;
RA   Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC   AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
CC   PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
CC   KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP

```
CC       INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC       PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC       INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC       AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
CC       ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC       VESSELS.
CC    -!- SUBCELLULAR LOCATION: Secreted.
CC    -!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
CC       ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC       TISSUES.
CC    -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC    -------------------------------------------------------------
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CC       or send an email to license@isb-sib.ch).
CC    -------------------------------------------------------------
DR       EMBL; D14874; BAA03589.1; -.
DR       EMBL; S73906; AAC60642.1; -.
DR       EMBL; D43639; BAA07756.1; ALT_SEQ.
DR       PIR; JN0476; JN0476.
DR       PIR; JN0684; JN0684.
DR       PIR; JC2351; JC2351.
DR       MIM; 103375; -.
DR       InterPro; IPR001710; Adrenomedullin.
DR       Pfam; PF02039; Adrenomedullin; 1.
DR       PRINTS; PR00801; ADRENOMEDULN.
KW       Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT       SIGNAL         1     21
FT       PEPTIDE       22     41      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT       PROPEP        45     92
FT       PEPTIDE       95    146      ADRENOMEDULLIN.
FT       PROPEP       148    185      PREPROAM C-TERMINAL FRAGMENT.
FT       DISULFID     110    115
FT       MOD_RES       41     41      AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT       MOD_RES      146    146      AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ       SEQUENCE     185 AA;    20420 MW;  64C7D2A0B4654DFE CRC64;

Query Match
Best Local Similarity  100.0%;    Score 947;  DB 1;  Length 185;
Matches 182; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy     1  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP   63

Qy    61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ  123

Qy   121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSGSAPH  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSGSAPH  183

Qy   181  FL  182
          ||
Db   184  FL  185

RESULT 2
ADML_PIG
ID   ADML_PIG      STANDARD;        PRT;      188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Sus scrofa (Pig).
```

```
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX       NCBI_TaxID=9823;
RN       [1]
RP       SEQUENCE FROM N.A.
RC       TISSUE=Adrenal medulla;
RX       MEDLINE=94139945; PubMed=8043068;
RA       Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT       "Complete amino acid sequence of porcine adrenomedullin and cloning
RT       of cDNA encoding its precursor.";
RL       FEBS Lett. 338:306-310(1994).
RN       [2]
RP       SEQUENCE OF 22-41.
RC       TISSUE=Adrenal medulla;
RX       MEDLINE=94357274; PubMed=8076689;
RA       Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA       Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT       "Identification and hypotensive activity of proadrenomedullin
RT       N-terminal 20 peptide (PAMP).";
RL       FEBS Lett. 351:35-37(1994).
CC    -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC    -!- SUBCELLULAR LOCATION: Secreted.
CC    -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC       KIDNEY.
CC    -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC    -------------------------------------------------------------
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CC    -------------------------------------------------------------
DR       EMBL; D14875; BAA03590.1; -.
DR       InterPro; IPR001710; Adrenomedullin.
DR       Pfam; PF02039; Adrenomedullin; 1.
DR       PRINTS; PR00801; ADRENOMEDULN.
KW       Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT       SIGNAL         1     21
FT       PEPTIDE       22     41      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT       PROPEP        45     92
FT       PEPTIDE       95    146      ADRENOMEDULLIN.
FT       PROPEP       153    188      PREPROAM C-TERMINAL FRAGMENT (BY
FT                                    SIMILARITY).
FT       DISULFID     110    115      BY SIMILARITY.
FT       MOD_RES       41     41      AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT       MOD_RES      146    146      AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ       SEQUENCE     188 AA;    20893 MW;  7174460F5660A61 CRC64;

Query Match
Best Local Similarity   86.3%;    Score 817;  DB 1;  Length 188;
Matches 156; Conservative  10; Mismatches   9; Indels   0; Gaps   0;

Qy     1  VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP   60
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4  VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSSYPTGIADLKAGP   63

Qy    61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ  120
          |||.||:||:|::||: ::|| :.||||||||||||||||||||||||||||||||||||
Db    64  AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ  123

Qy   121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS  175
          |||||||||| ||||||||||||||||||||||| ||| |:||||||| |:
Db   124  IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA  178

RESULT 3
ADML_BOVIN
ID   ADML_BOVIN    STANDARD;        PRT;      188 AA.
AC   O62827;
DT   16-OCT-2001 (Rel. 40, Created)
```

```
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC       CIRCULATION CONTROL (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
SQ   SEQUENCE   188 AA;  20981 MW;  3002E79AB3B6612C CRC64;

Query Match             81.8%;  Score 774.5;  DB 1;  Length 188;
Best Local Similarity   87.8%;  Pred. No. 2e-62;
Matches 151;  Conservative 7;  Mismatches 13;  Indels 1;  Gaps 1;

Qy     1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
           ||||||||||||||| ||||||| |||||||||||||||||| |||||||||||||||
Db     4 VPVALMYLGSLAFLGVDTARLDVAAEFRKKWNKWALSRGKRELRESSSYPTGLADVKAGP 63
Qy    61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||||:||||||||:  |||||||||||||||||:||||||||||||||||||||||
Db    64 VQTLIRPQDVKGASRSPQASSPDAARIRVKRYRQSLNNFQGLRSFGCRFGTCTVQKLAHQ 123
Qy   121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVS-SKPQAHGAP 171
         ||||| ||||  |||||||||||||||||||||||| ||||| :|: |||
Db   124 IYHFTDKDKDGAPRSKISPQGYGRRRRRSLPEAGLGRTLLQPPEPKLRGAP 175

RESULT 4
ADML_CANFA
ID   ADML_CANFA    STANDARD;   PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
```

```
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9902704; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; AF045773; AAD05423.1; -.
DR   EMBL; U96127; AAD09957.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   CONFLICT    130    130       N -> K (IN REF 2).
SQ   SEQUENCE   188 AA;  20929 MW;  80D6A64F98F5578 CRC64;

Query Match             81.4%;  Score 771;  DB 1;  Length 188;
Best Local Similarity   86.1%;  Pred. No. 4.2e-62;
Matches 149;  Conservative 10;  Mismatches 14;  Indels 0;  Gaps 0;

Qy     1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
           ||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||
Db     4 VPVALLYLGSLAFLGADTARLDVASEFRKKWNKWAVSRGKRELRVSSSYPTGLAEVKAGP 63
Qy    61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||.||:||||| .  |||||||||||||||||||||||||||||||||||||||||
Db    64 AQTLIRTQDVKGASRNPQTSGPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
Qy   121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
         ||||||:|||||||||||||||||||||||||| | || ||  |:   || ||
Db   124 IYQFTDNDKDGVAPRSKISPQGYGRRRRRSLPEPGLRRTLLFPEPRPGGAPAP 176

RESULT 5
ADML_RAT
ID   ADML_RAT      STANDARD;   PRT;   185 AA.
AC   P43145;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
```

DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX   MEDLINE=93384621; PubMed=7690563;
RA   Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA   Matsuo H., Eto T.;
RT   "Molecular cloning and biological activities of rat adrenomedullin, a
RT   hypotensive peptide.";
RL   Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96102137; PubMed=8524787;
RA   Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA   Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT   "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT   its role in exacerbating focal brain ischemic damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
     AGENTS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
     HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21   BY SIMILARITY.
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   91   BY SIMILARITY.
FT   PEPTIDE   94   143   ADRENOMEDULLIN.
FT   PROPEP   149   185   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   107   112   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   MOD_RES   143   143   AMIDATION (G-144 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
SQ   SEQUENCE   185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;

Query Match   65.9%; Score 624.5; DB 1; Length 185;
Best Local Similarity   72.0%; Pred. No. 5.1e-49;
Matches 126; Conservative 14; Mismatches 32; Indels 3; Gaps 2;

Qy   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
              ||:|||||:|||||||||||||:|||||||||||||||||||||||||||:||||||||||
Db   4 VSIALMLLGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVG 63

Qy   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
              ||| |:|: |::|:: :: |||||:||||||||:|:| |||||||||||||||||||||||
Db   64 TQTL-GLQDKQSTSSTPQASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQ 120

Qy   121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175

RESULT 6
ADML_MOUSE
ID   ADML_MOUSE   STANDARD;   PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RA   Yotsumoto S., Ko M.S.H.;
RT   "Expression of mouse adrenomedullin gene in trophoblastic giant
RT   cells at the implantation site.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
     AGENTS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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CC   or send an email to license@isb-sib.ch).

DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21   BY SIMILARITY.
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92   BY SIMILARITY.
FT   PEPTIDE   95   144   ADRENOMEDULLIN.
FT   PROPEP   151   184   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   108   113   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   MOD_RES   144   144   AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT   (BY SIMILARITY).
FT   CONFLICT   173   173   A -> G (IN REF. 2).
SQ   SEQUENCE   184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match   60.2%; Score 570; DB 1; Length 184;
Best Local Similarity   68.8%; Pred. No. 3.7e-44;
Matches 119; Conservative 11; Mismatches 41; Indels 2; Gaps 1;

Qy   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60

Db   121 IYQFTDKDKDQGMAPRNKISPQGYGRRRRRSLPEVLRARTVESSQEQTHSAPASPA 175

```
Db     4  VSITLMLLGSLAFLGADYTAGPDTPSQFRKKWNKWALSRGKRELQASSSYPTGLADETTVP   63
          ||:  ||: |||||||||||| ||||||||||||||||||||||: ||||||||||||
Qy    61  AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNFQGLRSFGCRFGTCTCVQKLAHQ  120
          |||  |: :|:  |||||||||||| ||| || ||||||||||||||| ||||||
Db    64  TQTLDPFLDEQNTGPLQASNQSEAHIRVKRYRQSMN-QGSRSNGCRFGTCTFQKLAHQ   121
          |||||| ||||: ||  ::|  |||||||||||| :||: |||||||||||||
Qy   121  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP       173
          |||| |||||||  ||||||||||||||||||||||: ||:|| ||
Db   122  IYQLTDKDKDGMAPRNKISPQGYGRRRRRSLLEVLRSRFTVESSSQEQTHTAPAP      174

RESULT 7
TTP_HUMAN
ID   TTP_HUMAN      STANDARD;      PRT;    326 AA.
AC   P26651;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Tristetraproline (TTP) (TIS11A protein) (TIS11) (ZFP-36) (Growth
DE   factor-inducible nuclear protein NUP475) (G0/G1 switch regulatory
DE   protein 24).
GN   ZFP36 OR TIS11A OR TTP OR G0S24.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91288233; PubMed=2062660;
RA   Taylor G.A., Lai W.S., Oakey R.J., Seldin M.F., Shows T.B.,
RA   Eddy R.L. Jr., Blackshear P.J.;
RT   "The human TTP protein: sequence, alignment with related proteins,
RT   and chromosomal localization of the mouse and human genes.";
RL   Nucleic Acids Res. 19:3454-3454(1991).
CC   -!- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
CC       STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
CC       HAS BEEN EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
CC   -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; M92843; AAA58489.1; -.
DR   EMBL; M92844; AAC37600.1; -.
DR   EMBL; M63625; AAA61240.1; -.
DR   PIR; S34427; S34427.
DR   MIM; 190700; -.
DR   InterPro; IPR000571; zf-CCCH.
DR   Pfam; PF00642; zf-CCCH; 2.
DR   SMART; SM00356; ZnF_C3H1; 2.
KW   Nuclear protein; Repeat; Metal-binding; Zinc-finger; DNA-binding.
FT   REPEAT        71     75       P-P-P-P-G.
FT   REPEAT       198    202       P-P-P-P-G.
FT   REPEAT       219    223       P-P-P-P-G.
FT   ZN_FING      109    128       C3H1-TYPE 1.
FT   ZN_FING      147    166       C3H1-TYPE 2.
SQ   SEQUENCE   326 AA;  34003 MW;  DDD9AD950AF7AF98 CRC64;

Query Match             9.5%;  Score 89.5;  DB 1;  Length 326;
Best Local Similarity   22.4%;  Pred. No. 0.61;
Matches   45;  Conservative  18;  Mismatches  77;  Indels  61;  Gaps   8;

Qy    34  WALSRGKRELRMSSSYPFTGLADVKAGPAQTLIRPQD----------------MKGASRSPE  78
          |       || ::|:|:|  ::|                              ||
Db    32  WG-SSGPWSLSPSDSSPSGVTSRLPGRSTSLVEGRSCGWVPPPGFAPLAPRLGPELSPS  90
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Qy    79  DSSPDAARIRVKRYRQSMNNFQGLRSFG----CRFGT-CTV---------------QK  116
          :||: |||||||||||| ::     ||    |:|    |:|
Db    91  PTSPTATSTTPSRYKTEL-----CRTFSESGCRYGACKCQFAHGLGELRQANRHPYKTE  145

Qy   117  LAHQIYQ-------------FTDKDKDNVAP----------RSKISPQGYGRRRRRSLPEAGPGR  158
          ||||| |             ||||||||||          |||||||||||||||||||||||
Db   146  LCHKFYLQGRCPYGSRCHFIHNPSEDLAAPGHPPVLRQSISFSGLPSGRRTSPPPPGLAG  205

Qy   159  TLVSSKPQAHGAPAPPSGSAP  179
          :|| |||||||||||||||
Db   206  PSLSSSSFSPSSSPPPPGDLP  226

RESULT 8
FA5_HUMAN
ID   FA5_HUMAN      STANDARD;      PRT;   2224 AA.
AC   P12259; Q14285;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Coagulation factor V precursor (Activated protein C cofactor).
GN   F5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92232668; PubMed=1567832;
RA   Cripe L.D., Moore K.D., Kane W.H.;
RT   "Structure of the gene for human coagulation factor V.";
RL   Biochemistry 31:3777-3785(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87260886; PubMed=3110773;
RA   Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
RA   Hewick R.M., Kaufman R.J., Mann K.G.;
RT   "Complete cDNA and derived amino acid sequence of human factor V.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
RN   [3]
RP   SEQUENCE OF 1-1600 FROM N.A.
RX   MEDLINE=88107560; PubMed=2827731;
RA   Kane W.H., Ichinose A., Hagen F.S., Davie E.W.;
RT   "Cloning of cDNAs coding for the heavy chain region and connecting
RT   region of human factor V, a blood coagulation factor with four types
RT   of internal repeats.";
RL   Biochemistry 26:6508-6514(1987).
RN   [4]
RP   SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A.
RX   MEDLINE=86313665; PubMed=3092220;
RA   Kane W.H., Davie E.W.;
RT   "Cloning of a cDNA coding for human factor V, a blood coagulation
RT   factor homologous to factor VIII and ceruloplasmin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
RN   [5]
RP   PARTIAL SEQUENCE FROM N.A.
RC   TISSUE=Fibroblast;
RX   MEDLINE=93203619; PubMed=8454869;
RA   Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
RA   Edgington T.S.;
RT   "The serine protease cofactor factor V is synthesized by
RT   lymphocytes.";
RL   J. Immunol. 150:2992-3001(1993).
RN   [6]
RP   SULFATION.
RX   MEDLINE=94264012; PubMed=8204629;
RA   Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
RA   Kaufman R.J.;
RT   "Posttranslational sulfation of factor V is required for efficient
RT   thrombin cleavage and activation and for full procoagulant activity.";
RL   Biochemistry 33:6952-6959(1994).
RN   [7]
```

```
RP   SULFATION.
RX   MEDLINE=90366699; PubMed=2168225;
RA   Hortin G.L.;
RT   "Sulfation of tyrosine residues in coagulation factor V.";
RL   Blood 76:946-952(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
RX   MEDLINE=20052169; PubMed=10586886;
RA   Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
RA   Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
RA   Fuentes-Prior P.;
RT   "Crystal structures of the membrane-binding C2 domain of human
RT   coagulation factor V.";
RL   Nature 402:434-439(1999).
RN   [9]
RP   VARIANT APCR GLN-534.
RX   MEDLINE=94217810; PubMed=8164741;
RA   Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
RA   Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
RT   "Mutation in blood coagulation factor V associated with resistance to
RT   activated protein C.";
RL   Nature 369:64-67(1994).
CC   -!- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
CC       WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
CC   -!- SUBUNIT: Factor Va is composed of a heavy chain and a light
CC       chain, noncovalently bound. The interaction between the two chains
CC       is calcium-dependent.
CC   -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
CC       REPEATS.
CC   -!- PTM: Thrombin activates factor V proteolytically to the active
CC       cofactor, factor Va (formation of a heavy chain at the N-
CC       terminus and a light chain at the C-terminus).
CC   -!- PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND
CC       ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.
CC   -!- DISEASE: OWREN PARAHEMOPHILIA, AN HEMORRHAGIC DIASTESIS, IS DUE
CC       TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN F5 RESULTS IN A
CC       FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
CC       MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT
CC       A SLIGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
CC       IMPLANTATION.
CC   -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
CC       2 PLASTOCYANIN-LIKE REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC   -!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
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CC   --------------------------------------------------------------------------
DR   EMBL; L32779; AAB59401.1; -.
DR   EMBL; L32755; AAB59401.1; JOINED.
DR   EMBL; L32756; AAB59401.1; JOINED.
DR   EMBL; L32757; AAB59401.1; JOINED.
DR   EMBL; L32758; AAB59401.1; JOINED.
DR   EMBL; L32759; AAB59401.1; JOINED.
DR   EMBL; L32760; AAB59401.1; JOINED.
DR   EMBL; L32761; AAB59401.1; JOINED.
DR   EMBL; L32762; AAB59401.1; JOINED.
DR   EMBL; L32763; AAB59401.1; JOINED.
DR   EMBL; L32764; AAB59401.1; JOINED.
DR   EMBL; L32765; AAB59401.1; JOINED.
DR   EMBL; L32766; AAB59401.1; JOINED.
DR   EMBL; L32767; AAB59401.1; JOINED.
DR   EMBL; L32768; AAB59401.1; JOINED.
DR   EMBL; L32769; AAB59401.1; JOINED.
DR   EMBL; L32770; AAB59401.1; JOINED.
DR   EMBL; L32771; AAB59401.1; JOINED.
DR   EMBL; L32772; AAB59401.1; JOINED.
DR   EMBL; L32773; AAB59401.1; JOINED.
DR   EMBL; L32774; AAB59401.1; JOINED.
DR   EMBL; L32775; AAB59401.1; JOINED.
DR   EMBL; L32777; AAB59401.1; JOINED.
DR   EMBL; L32778; AAB59401.1; JOINED.
DR   EMBL; M16967; AAA52424.1; -.
DR   EMBL; M14335; AAB59532.1; -.
DR   PIR; A25897; A25897.
DR   PIR; A28028; A28028.
DR   PDB; 1CZS; 26-NOV-99.
DR   PDB; 1CZT; 26-NOV-99.
DR   PDB; 1CZV; 26-NOV-99.
DR   MIM; 134400; -.
DR   MIM; 188055; -.
DR   MIM; 227310; -.
DR   MIM; 227400; -.
DR   InterPro; IPR001117; Cu-oxidase.
DR   InterPro; IPR000421; FA58_C.
DR   Pfam; PF00394; Cu-oxidase; 3.
DR   Pfam; PF00754; F5_F8_type_C; 2.
DR   SMART; SM00231; FA58C; 2.
DR   PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR   PROSITE; PS01285; FA58C_1; 2.
DR   PROSITE; PS01286; FA58C_2; 2.
KW   Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
KW   Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
FT   SIGNAL          1     28
FT   CHAIN          29   2224       COAGULATION FACTOR V.
FT   CHAIN          29    737       HEAVY CHAIN.
FT   PEPTIDE       738   1573       ACTIVATION PEPTIDE (CONNECTING REGION).
FT   CHAIN        1574   2224       LIGHT CHAIN.
FT   DOMAIN         30    329       F5/8 TYPE A 1.
FT   DOMAIN         30    193       PLASTOCYANIN-LIKE 1.
FT   DOMAIN        203    329       PLASTOCYANIN-LIKE 2.
FT   DOMAIN        348    684       F5/8 TYPE A 2.
FT   DOMAIN        348    526       PLASTOCYANIN-LIKE 3.
FT   DOMAIN        536    684       PLASTOCYANIN-LIKE 4.
FT   DOMAIN        692   1573       B.
FT   DOMAIN        895    928       2 X 17 AA TANDEM REPEATS.
FT   REPEAT        895    911       1-1.
FT   REPEAT        912    928       1-2.
FT   SIMILAR      1135   1148       TO 14 AA REPEATS IN BOVINE FA5.
FT   DOMAIN       1185   1501       35 X 9 AA APPROXIMATE TANDEM REPEATS OF
FT                                  [TNP]-L-S-P-D-L-S-Q-T.
FT   REPEAT       1185   1193       2-1.
FT   REPEAT       1194   1202       2-2.
FT   REPEAT       1203   1211       2-3.
FT   REPEAT       1212   1220       2-4.
FT   REPEAT       1221   1229       2-5.
FT   REPEAT       1230   1238       2-6.
FT   REPEAT       1239   1247       2-7.
FT   REPEAT       1248   1256       2-8.
FT   REPEAT       1257   1265       2-9.
FT   REPEAT       1266   1274       2-10.
FT   REPEAT       1275   1283       2-11.
FT   REPEAT       1284   1292       2-12.
FT   REPEAT       1293   1301       2-13.
FT   REPEAT       1302   1310       2-14.
FT   REPEAT       1311   1319       2-15.
FT   REPEAT       1320   1328       2-16.
FT   REPEAT       1329   1337       2-17.
FT   REPEAT       1338   1346       2-18.
FT   REPEAT       1347   1355       2-19.
FT   REPEAT       1356   1364       2-20.
FT   REPEAT       1365   1373       2-21.
FT   REPEAT       1374   1382       2-22.
FT   REPEAT       1383   1391       2-23.
FT   REPEAT       1392   1400       2-24.
FT   REPEAT       1401   1409       2-25.
FT   REPEAT       1410   1418       2-26.

Query Match            9.4%;      Score 89; DB 1; Length 2224;
Best Local Similarity 23.2%;      Pred. No. 6;
```

Matches   39; Conservative   26; Mismatches   71; Indels   32; Gaps   5;

```
Qy       3 VALMYLGSLAFLGADTAR------LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD   55
           :|  |: |:. .|:             |: :||:|||
Db     847 IRLLSLGAGEFKSQEHAKHKGPKVERDQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRP  906

Qy      56 VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT  111
           :  |||  |  ||| |  ||           | |||||||||||||||||||||||||||
Db     907 WEDLPSQDTGPSPSRMRPWKDPPDSDLLLKQSNSSKILVGRWHLAS------------  951

Qy     112 CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-PGR  158
           |||||||||||   .|  ::|:|   ||  ||  |||  |||||  ||
Db     952 ---EKGSYEIIQ--DTDEDTAVNNWLISPQNASRAWGESTPLANKPGK  994
```

RESULT 9

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CEFD_STRCL
ID   CEFD_STRCL          STANDARD;       PRT;    397 AA.
AC   P18549;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Isopenicillin N epimerase (EC 5.-.-.-).
GN   CEFD.
OS   Streptomyces clavuligerus.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1901;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
RX   MEDLINE=90299822; PubMed=1694525;
RA   Kovacevic S., Tobin M.B., Miller J.R.;
RT   "The beta-lactam biosynthesis genes for isopenicillin N epimerase and
RT   deacetoxycephalosporin C synthetase are expressed from a single
RT   transcript in Streptomyces clavuligerus.";
RL   J. Bacteriol. 172:3952-3958(1990).
RN   [2]
RP   SEQUENCE OF 1-23.
RX   MEDLINE=90028393; PubMed=2804141;
RA   Usul S., Yu C.-A.;
RT   "Purification and properties of isopenicillin N epimerase from
RT   Streptomyces clavuligerus.";
RL   Biochim. Biophys. Acta 999:78-85(1989).
CC   -!- FUNCTION: CATALYZES THE REVERSIBLE ISOMERIZATION BETWEEN
CC       ISOPENICILLIN N AND PENICILLIN N.
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- PATHWAY: BIOSYNTHESIS OF CEPHALOSPORIN ANTIBIOTICS.
CC   -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC       AMINOTRANSFERASES.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M32324; AAA26714.1; -.
DR   InterPro; IPR000192; Aminotransf_class_V.
DR   Pfam; PF00266; aminotran_5; 1.
DR   PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW   Antibiotic biosynthesis; Isomerase; Pyridoxal phosphate.
FT   INIT_MET      0      0
FT   BINDING     216    216       PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ   SEQUENCE   397 AA;  43366 MW;  A15274189H192FF CRC64;
```

Query Match   9.3%; Score 88.5; DB 1; Length 397;
Best Local Similarity 24.7%; Pred. No. 0.94;
Matches   46; Conservative   20; Mismatches   63; Indels   57; Gaps   11;

```
Qy      13 FLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQ-TLIRPQDMK   71
```

```
Db     197 FLDLDLSRIP-CDFYAGSGHKWLLA---------------PTGVGFLHLAPGRLELEPTQVS  243
           ||:. |::|:                                ||| .|||  . :| |
Qy      72 GASRSPEDSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT------CTVQKLAHQIYQF  124
           |:    | :|| | :| :: |   .|   |||:||||||||
Db     244 WAYEPPEGSGPPAARDR------FGSTPGLRRLECE-GTRDICPWLATPESIDFQ----  291
           | | |  | |||||||        || ||:|| ||   | | ||| |  |   |
Qy     125 TDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-----PGRTLVS-SKPQAHGAPA----  172
           ||||||||||||||||||||||||||      ||   |: :.| .|  |
Db     292 ---------------------AELGP-GAIRARRELTDHARRLLADRPGRTLLTPDSPELSGGMVAYRL  339

Qy     173 PPSGSA  178
           || ||
Db     340 PPGTDA  345
```

RESULT 10

```
A2AA_MOUSE
ID   A2AA_MOUSE          STANDARD;       PRT;    450 AA.
AC   Q01338;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
GN   ADRA2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92342131; PubMed=1353249;
RA   Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
RT   "Cloning of two mouse genes encoding alpha 2-adrenergic receptor
RT   subtypes and identification of a single amino acid in the mouse alpha
RT   2-C10 homolog responsible for an interspecies variation in
RT   antagonist binding.";
RL   Mol. Pharmacol. 42:16-27(1992).
CC   -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC       INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC       PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M99377; AAA37213.1; -.
DR   HSSP; P29274; 1MMH.
DR   GCRDb; GCR_0439; -.
DR   MGD; MGI:87934; Adra2a.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     96       2 (POTENTIAL).
FT   DOMAIN       97    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    173       4 (POTENTIAL).
FT   DOMAIN      174    192       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    193    217       5 (POTENTIAL).
```

```
FT   DOMAIN      218    374       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    375    399       6 (POTENTIAL).
FT   DOMAIN      400    409       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    410    430       7 (POTENTIAL).
FT   DOMAIN      431    450       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    10     10        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    14     14        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    188       BY SIMILARITY.
FT   LIPID       442    442       PALMITATE (BY SIMILARITY).
FT   SITE        113    113       IMPLICATED IN LIGAND BINDING (BY
FT                                SIMILARITY).
FT   SITE        200    200       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   SITE        204    204       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
SQ   SEQUENCE    450 AA;  48865 MW;  F07E225393AFA93B CRC64;
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Query Match        9.2%;  Score 87;  DB 1;  Length 450;
Best Local Similarity  28.9%;  Pred. No. 1.5;
Matches   35;  Conservative  14;  Mismatches  54;  Indels  18;  Gaps  6;

Qy    69  DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK  127
              :|||  .:::||       |||||:      :::|||
Db   173  EKKGAGGGQPAEPSCKINDQKWVIS-------SSIGSFFAPCLIMILVYVRIYQIA-K  224

Qy   128  DKDNVAPRSK-----ISPQGYGRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA  178
              :|:|   ||  || | |   :|||  |:  ||||
Db   225  RRTRVPPSRRGPDACSAPPGGADRRPNGLGPERGAGPTGAEAEPLPTQLNGAPGEPAPAG  284

Qy   179  P  179
          |
Db   285  P  285
```

RESULT 11
DNAA_STRCO
```
ID   DNAA_STRCO     STANDARD;      PRT;   656 AA.
AC   P27902; Q9KXX4;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Chromosomal replication initiator protein dnaA.
GN   DNAA OR SCH18.16C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=92250416; PubMed=1577691;
RA   Calcutt M.J., Schmidt F.J.;
RT   "Conserved gene arrangement in the origin region of the Streptomyces
RT   coelicolor chromosome.";
RL   J. Bacteriol. 174:3220-3226(1992).
RN   [2]
RP   SEQUENCE OF 51-656 FROM N.A.
RC   STRAIN=A3(2);
RA   Brown S.P., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
RA   Rajandream M.A.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
CC       OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION;
CC       IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS
CC       (DNAA BOX): 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO
CC       ACIDIC PHOSPHOLIPIDS.
CC   -!- SIMILARITY: BELONGS TO THE DNAA FAMILY.
CC       -----------------------------------------------------------------
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CC       -----------------------------------------------------------------
DR   EMBL; AF187159; AAA26734.1; -.
DR   EMBL; AL357152; CAB92999.1; -.
DR   PIR; A41870; A41870.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001957; Bac_DnaA.
DR   Pfam; PF00308; bac_dnaA; 1.
DR   PRINTS; PR00051; DNAA.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS01008; DNAA; 1.
KW   DNA replication; DNA-binding; ATP-binding.
FT   NP_BIND     357    364       ATP (POTENTIAL).
SQ   SEQUENCE    656 AA;  73182 MW;  6C1D5C0193D3C92B CRC64;
```

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Query Match        9.2%;  Score 87;  DB 1;  Length 656;
Best Local Similarity  25.4%;  Pred. No. 2.3;
Matches   43;  Conservative  16;  Mismatches  64;  Indels  46;  Gaps  6;

Qy    14  LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA  73
              |  ||| |    ||    |  ::  |     |::    .|||||::||||
Db    44  LVDATALLAVPNEFAK-------GVLEGRLAPIVSETLSRECGRPIRIAITVVDDTAGE  94

Qy    74  SRSPEDSSPDAARIRVK-RYRQS-MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD  130
              ::   :|::  :  ||      ||| | |::::|    ||:
Db    95  PAGPAPQAPQSPPSRPQHRYEEPELPAPGQGGRE-------------EYRDRDE-  135

Qy   131  NVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP  179
              :|    |||     ||  ||
Db   136  ------YEGYGRNRADQLPTARP------AYPQEYQRPEPGSWPRP  169
```

RESULT 12
MPI2_RAT
```
ID   MPI2_RAT       STANDARD;      PRT;   574 AA.
AC   P48966;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   M-phase inducer phosphatase 2 (EC 3.1.3.48) (Dual specificity
DE   phosphatase Cdc25B).
GN   CDC25B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRK49F;
RX   MEDLINE=94208523; PubMed=8156993;
RA   Jinno S., Suto K., Nagata A., Igarashi M., Kanaoka Y., Nojima H.,
RA   Okayama H.;
RT   "Cdc25A is a novel phosphatase functioning early in the cell cycle.";
RL   EMBO J. 13:1549-1556(1994).
CC   -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
CC       MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
CC       PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
CC       P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- ENZYME REGULATION: STIMULATED BY CYCLINS B.
CC   -!- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
CC       AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
CC       -----------------------------------------------------------------
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CC       or send an email to license@isb-sib.ch).
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DR   EMBL; D16237; BAA03762.1; -.
DR   HSSP; P30305; 1QB0.
DR   InterPro; IPR000751; MPI_Phosphatase.
DR   InterPro; IPR001763; Rhodanese_domain.
DR   Pfam; PF00581; Rhodanese; 1.
DR   PRINTS; PR00716; MPIPHPHTASE.
DR   SMART; SM00450; RHOD; 1.
KW   Cell division; Mitosis; Hydrolase; Multigene family.
FT   ACT_SITE      481    481       BY SIMILARITY.
SQ   SEQUENCE   574 AA;  64286 MW;  9367CE203B15FAAD CRC64;

Query Match             8.8%;  Score 83.5;  DB 1;  Length 574;
Best Local Similarity  23.3%;  Pred. No. 4;
Matches   47;  Conservative   23;  Mismatches   79;  Indels   53;  Gaps   7;

Qy      6 MYLGSLAFLGADTARLDVAS-EFRKKWNKWALSRGKRELRMSSSYYPTGLADVKAGPAQTL 64
          ||  :||:|||  |  ||  : |  |  |||:||| : :||     |||  ||  ||
Db     59 MY--NLAGLGSETPKIQVGSLSFQNRLTDLSLSRRTSECSLSSE---SSESSDAGLCMDS 113

Qy     65 IRPQDMKGASRSPEDSSPDAARIRVKR---------------------YRQSMNNFQGLRSFG 106
          ||  |  |:| :  :||:|     |   |                    : ||: || : ||
Db    114 PSPMDPQTAERTFEQAIQAASRVIQKMQFTIKASVFASEAAGHSPVLQNITNSQALDSW- 172

Qy    107 CRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISP-------QGYGRRRRRSLPEAGPGRTL 160
          | :    |:|    | | |  | | :  :|  |         |  ||||||  | |  |
Db    173 --------------------------------------EKDEAGYRAASSPGEDKENDGYIFKMPQKLPHSSSARAL 211

Qy    161 VSSKPQAHGAPAPPSGSGAPHFL 182
           : :| |:  ||  ||||:|
Db    212 AEWASRREAFTQRPS-SAPDLM 232
```

RESULT 13

```
A2AA_RAT
ID   A2AA_RAT      STANDARD;      PRT;   450 AA.
AC   P22909;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
DE   (CA2-47) (Alpha-2D adrenergic receptor).
GN   ADRA2A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91244823; PubMed=1645350;
RA   Lanier S.M., Downing S., Duzic E., Homcy C.J.;
RT   "Isolation of rat genomic clones encoding subtypes of the alpha 2-
RT   adrenergic receptor. Identification of a unique receptor subtype.";
RL   J. Biol. Chem. 266:10470-10478(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91125329; PubMed=2177834;
RA   Chalberg S.C., Duda T., Rhine J.A., Sharma R.K.;
RT   "Molecular cloning, sequencing and expression of an alpha 2-adrenergic
RT   receptor complementary DNA from rat brain.";
RL   Mol. Cell. Biochem. 97:161-172(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95349560; PubMed=7623790;
RA   Wyplewski K., Duda T., Sharma R.K.;
RT   "Structural, genetic and pharmacological identity of the rat alpha
RT   2-adrenergic receptor subtype CA2-47 and its molecular
RT   characterization in rat adrenal, adrenocortical carcinoma and bovine
RT   retina.";
RL   Mol. Cell. Biochem. 144:181-190(1995).
CC   -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC       INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC       PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
```

```
DR   EMBL; M62372; AAA42034.1; -.
DR   EMBL; U79031; AAC24959.1; -.
DR   PIR; B40392; B40392.
DR   PIR; JH0190; JH0190.
DR   HSSP; P29274; 1MMH.
DR   GCRDb; GCR_0154; -.
DR   GCRDb; GCR_0200; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     96       2 (POTENTIAL).
FT   DOMAIN       97    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    173       4 (POTENTIAL).
FT   DOMAIN      174    192       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    193    217       5 (POTENTIAL).
FT   DOMAIN      218    374       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    375    399       6 (POTENTIAL).
FT   DOMAIN      400    409       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    410    430       7 (POTENTIAL).
FT   DOMAIN      431    450       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     14     14       N-LINKED (GLCNAC...) (POTENTIAL).
FT   DISULFID    106    188       BY SIMILARITY.
FT   LIPID       442    442       PALMITATE (BY SIMILARITY).
FT   SITE        113    113       IMPLICATED IN LIGAND BINDING (BY
FT                                SIMILARITY).
FT   SITE        200    200       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   SITE        204    204       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   CONFLICT    147    147       P -> R (IN REF. 2).
FT   CONFLICT    154    158       IVIVW -> HCHCV (IN REF. 2).
FT   CONFLICT    252    253       GL -> AV (IN REF. 1).
FT   CONFLICT    264    264       A -> G (IN REF. 2).
FT   CONFLICT    304    305       RP -> PR (IN REF. 1).
FT   CONFLICT    333    333       P -> R (IN REF. 1).
FT   CONFLICT    445    445       D -> N (IN REF. 2).
SQ   SEQUENCE   450 AA;  48939 MW;  AFA078DCA3D612AC CRC64;

Query Match             8.7%;  Score 82;  DB 1;  Length 450;
Best Local Similarity  28.1%;  Pred. No. 4.1;
Matches   34;  Conservative   14;  Mismatches   55;  Indels   18;  Gaps   6;

Qy     69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
          :  ||| |  |||:|||||||:||| :|::|||||    :|:||| || | | |  | |
Db    173 EKKGAGGGQOPABPSCKINDQKWYVIS------SSIGSFFAPCLIMILVVRIYQIA-K 224

Qy    128 DKDNVAPRSK-----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP--QAHGAPAPPSGSGA 178
          || ||| |       ||| ||  |    |   |:|| |:   ::    ||| || : :|
Db    225 RRTRVPPSRRGPDACSAPPGGADRRPNGLGPERGAGTAGAEAEPLPTQLNGAPGEPAPTR 284

Qy    179 P 179
          |
Db    285 P 285
```

RESULT 14
TBR1_HUMAN
```
ID   TBR1_HUMAN    STANDARD;      PRT;   682 AA.
AC   Q16650;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-brain-1 protein (T-box brain protein 1) (TBR-1) (TES-56).
GN   TBR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=95344783; PubMed=7615531;
RA   Bulfone A., Smiga S.M., Shimamura K., Peterson A., Puelles L.,
RA   Rubenstein J.L.R.;
RT   "T-brain-1: a homolog of Brachyury whose expression defines
RT   molecularly distinct domains within the cerebral cortex.";
RL   Neuron 15:63-78(1995).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. TBR1 IS REQUIRED FOR NORMAL BRAIN
CC       DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: BRAIN.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; U49250; AAA92010.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 604616; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DNA_BIND    213    393    T-BOX.
FT   DOMAIN      569    573    POLY-ALA.
SQ   SEQUENCE   682 AA;  74053 MW;  E1C8D84206EFBBB5 CRC64;

Query Match   8.5%;  Score 80.5;  Pred. No. 9;  DB 1;  Length 682;
Best Local Similarity   23.9%;
Matches 34;  Conservative 18;  Mismatches 59;  Indels 31;  Gaps 4;

Qy   40 KRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNF 99
          |: | :|||||     :| :::|::  :  : :|||   :   ||||||:||
Db   15 KKFLNVSSSYP-----HSGGSELVLHDHPIISTTDNLERSSP------LKKITRGWTNQ 62

Qy  100 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG-RRRRRSLPEAGPGR 158
          |||:|| :   | ||||||||||||||||||||||||||||    |||||| | | |
Db   63 SDTDNFP---------------DSKDSPGDVQRSKLSPVLDGVSELRHSFDGSAADR 104

Qy  159 TLVSSKPQAHGAPAPPSGSAPH 180
          |:| :  ||  | :||
Db  105 YLLSQSSQPQSAATAPSAMFPY 126
```

RESULT 15
REPA_AGRTU
```
ID   REPA_AGRTU    STANDARD;      PRT;   250 AA.
AC   P15394;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-NOV-1990 (Rel. 16, Last annotation update)
DE   Replicating protein.
GN   REPA.
OS   Agrobacterium tumefaciens.
OG   Plasmid pTAR.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88257036; PubMed=3290199;
RA   Gallie D.R., Kado C.I.;
RT   "Minimal region necessary for autonomous replication of pTAR.";
RL   J. Bacteriol. 170:3170-3176(1988).
CC   -!- FUNCTION: REQUIRED FOR REPLICATION. IT LIKELY REGULATES PTAR
CC       COPY NUMBER.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M21299; AAD15307.1; -.
DR   PIR; A43662; A43662.
KW   Plasmid; DNA replication.
SQ   SEQUENCE   250 AA;  27987 MW;  CCED10653483197 9 CRC64;

Query Match   8.4%;  Score 80;  Pred. No. 3.2;  DB 1;  Length 250;
Best Local Similarity   27.2%;
Matches 52;  Conservative 24;  Mismatches 65;  Indels 50;  Gaps 12;

Qy    5 LMYLGGSLAFLGADTARLDVA-SEFRKKWNKWALSRGKRELRMSSSY------PTGLAD 55
          | | : ||        :  | |:      :|:|          |  :  |  | ||
Db   75 LDYLTNLVDFG--NGRLDPSISTIMEK------IGRAESCMSALYPNRQRGRRPAGAAD 125

Qy   56 VKAGPAQTL-IRPQDMKG-----ASRSPEDSSPDAARIR-----VKRYRQSMNNFQGLR 103
          |                |:: |                  ||: :|
Db  126 KQRLPEPAGARPRALLGKYVRKAAPLPD---DAAQARQERHDTIKAHMDSLSPADRLR 181

Qy  104 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGVGRRRRRS----LPEAGPGR 158
          |                :                 |||||:|:||::|     ||:|||
Db  182 E------TVEDRTRAEQLAGYVER---AAQNRPSGPRKAARRQQSRCSFTTPNR-PRR 230

Qy  159 TLVSSKPQAHG 169
          || || || |
Db  231 TLPSSHPQKFG 241

Search completed: October 17, 2002, 15:21:38
Job time : 11.4853 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:13 ; Search time 17.1922 Seconds
                                         (without alignments)
                                         1017.222 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence: 1 VSVALMYLGSLAFLGADTAR..........SKPQAHGAPAPPSGSAPHFL 182

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_71:*
                1: Pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	947	100.0	185	2	JN0684	adrenomedullin pre
2	817	86.3	188	2	S41600	adrenomedullin - p
3	624.5	65.9	185	2	JN0766	adrenomedullin pre
4	95.5	10.1	1116	2	T16112	hypothetical prote
5	89.5	9.5	326	2	S34427	tristetraproline p
6	89	9.4	2224	1	KFHU5	coagulation factor
7	88.5	9.3	398	2	T52311	isopenicillin N ep
8	87	9.2	450	2	I49481	alpha-2 adrenergic
9	87	9.2	656	2	A41870	dnaA protein - Str
10	83.5	8.8	560	2	T29586	hypothetical prote
11	83.5	8.8	574	2	I66868	cdc25B - rat
12	83	8.8	1051	2	C95367	conserved hypothet
13	83	8.8	450	2	JH0190	alpha-2-adrenergic
14	82.5	8.7	926	2	F88632	protein F56B3.4 [1
15	81.5	8.6	450	2	B40392	alpha-2-adrenergic
16	81	8.6	250	2	A43662	replicating protei
17	80	8.4	458	2	S24457	hypothetical prote
18	80	8.4	749	2	I37356	epithelial microtu
19	79	8.3	320	2	JC1255	TIS11 protein - ra
20	79	8.3	383	2	T39597	probable inositol
21	79	8.3	450	2	A34169	alpha-2A-adrenergi
22	78.5	8.3	481	1	B43674	protein kinase (EC
23	78.5	8.3	1196	2	T14108	SH3-containing pro
24	78.5	8.3	1224	2	S28368	hypothetical prote
25	78.5	8.3	1796	2	S65004	probable membrane
26	78.5	8.3	2145	2	JC4747	adenylate cyclase
27	78	8.2	519	1	FOLJG4	gag polyprotein -
28	78	8.2	678	2	JC4245	transcription fact
29	77.5	8.2	199	2	T36622	hypothetical prote
30	77.5	8.2	553	2	T27245	hypothetical prote
31	77.5	8.2	568	2	H88904	protein Y57G11C.9
32	77.5	8.2	659	2	T27246	hypothetical prote
33	77.5	8.2	723	2	AC1241	polynucleotide pho
34	77.5	8.2	1382	2	S70310	hypothetical prote
35	77.5	8.2	1681	2	S59693	hypothetical prote
36	77.5	8.2	1859	2	S63325	probable membrane
37	77.5	8.2	1859	2	S64633	probable membrane
38	77	8.1	591	2	S44203	parathyroid hormon
39	77	8.1	860	2	T35971	conserved hypothet
40	76.5	8.1	294	2	E88640	protein F55A8.1 [i
41	76.5	8.1	327	2	T02286	hypothetical prote
42	76.5	8.1	450	2	A38316	alpha-2-adrenergic
43	76.5	8.1	681	2	I78558	hypothetical Brach
44	76.5	8.1	2374	2	T21052	hypothetical prote
45	76	8.0	327	2	AG3448	transcription regu

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A;Reference number: JN0684; MUID:93343928
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-550, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A;Reference number: JN0476; MUID:93249425
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
F;1-21/Product: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match   100.08%;   Score 947; DB 2; Length 185;
Best Local Similarity 100.08%;   Pred. No. 5.2e-80;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

Qy  61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy 121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSGAPH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSGAPH 183

Qy 181 FL 182
        ||
Db 184 FL 185
```

RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encc
A;Reference number: S41600; MUID:94139945
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

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Query Match      86.3%;  Score 817;  DB 2;  Length 188;
Best Local Similarity   89.1%;  Pred. No. 5.1e-68;
  Matches 156;  Conservative 10;  Mismatches 9;  Indels 0;  Gaps 0;

Qy   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
        | |||||||||||||||||||||||||||||||||||||||||| :|||||:||||||
Db   4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63

Qy  61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
        |||||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||
Db  64 AQTVIRPQDVKGSSRSRPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy 121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
        ||||||||| |||||||||||||||||||||||||||       |||||||||
Db 124 IYQFTDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178
```

RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, I
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>

F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

```
Query Match      65.9%;  Score 624.5;  DB 2;  Length 185;
Best Local Similarity   72.0%;  Pred. No. 2.8e-50;
  Matches 126;  Conservative 14;  Mismatches 32;  Indels 3;  Gaps 2;

Qy   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
        ||:||| |||||| :|:|||||| :|:||||||||||||||||| :|||||||| |:|
Db   4 VSIALMLLGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP 63

Qy  61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
        |||| |:|||||  | :|  ||:  | |:|||||||||||:||||  ||||||| |||||
Db  64 TQTL-GLQDKQSTSSTPQASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQ 120

Qy 121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
        |||||||| :||:| ||:||||:|||||||||:  |:||:|| |:|    |||||
Db 121 IYQFTDKDKDGMAPRNKISPQGYGRRRRRSLPEVLRARTVESSQEQTHSAPASPA 175
```

RESULT 4
T16112
hypothetical protein F20D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16112
R;Wu, X.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F20D12.
A;Reference number: 218462
A;Accession: T16112
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1116 <WUX>
A;Cross-references: EMBL:U40933; NID:g1072142; PID:g1072146; PIDN:AAA81675.1; CESP:F2
C;Genetics:
C;Gene: CESP:F20D12.2
A;Introns: 21/1; 85/1; 175/3; 217/1; 361/3; 697/3; 891/1; 1008/1; 1072/1

```
Query Match      10.1%;  Score 95.5;  DB 2;  Length 1116;
Best Local Similarity   22.2%;  Pred. No. 1.2;
  Matches 36;  Conservative 26;  Mismatches 63;  Indels 37;  Gaps 6;

Qy  46 SSSYP-TGLADVKA--------GPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQ 94
        ::|| | :| ||                      :  :          :::
Db  73 TSSFPLKGSGDTKVPNLREGEFAIRPRQRMIPPAGANSLFRRPREGTPDGSENRNTNFQK 132

Qy  95 SMNNFQG--------------LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK 137
        :|:| :            ||   ||   :: :
Db 133 NLNDIKSEAPLGKVNFSQFGRKDEIKSF---FGRAK-PKIEEESIDETDHVIKKEAPPSM 188

Qy 138 I-----SPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPP 174
        |     |||||||||||||||||||||||||||||
Db 189 FGVTLAAPKGFGSISSLTEKPSSSIKSFGSWKPSSRSSPAPP 230
```

RESULT 5
S34427
tristetraproline protein - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S34427
R;Taylor, G.A.; Lai, W.S.; Oakey, R.J.; Seldin, M.F.; Shows, T.B.; Eddy Jr., R.L.; Bl
Nucleic Acids Res. 19, 3454, 1991
A;Title: The human TTP protein: sequence, alignment with related proteins, and chromo
A;Reference number: S34427; MUID:91288233
A;Accession: S34427
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-326 <TAY>
A;Cross-references: EMBL:M63625; NID:g340012; NID:g340013; PIDN:AAA61240.1; PID:g340013
C;Keywords: DNA binding

```
Query Match    9.5%;  Score 89.5;  DB 2;  Length 326;
Best Local Similarity  22.4%;  Pred. No. 1.1;
Matches  45;  Conservative  18;  Mismatches  77;  Indels  61;  Gaps  8;

Qy   34  WALSRGKRELRMSSSYPTGLADVVKAGPAQTLIRPQD----------MKGASRSPE  78
             | :::| |:::|:|| :  |  |:|                              ||
Db   32  WG--SGPWSLSPSDSSPPSGVTSRLPGRSTSLVEGRSCGWVPPPGFAPLAPRLGPELSPS  90

Qy   79  DSSPDAARIRVKRYRQSMNNFQGLRSFG---CRFGT-CTV---------QK 116
             |||  ||  ||:  ||     :||      :||:      :
Db   91  PTSPTATSTTPSRYKTEL----CRTFSESGRCRYGAKCQFAHGLGELRQANRHPKYKTE 145

Qy  117  LAHQIYQ----------FTDKDKDNVAP------RSKISPQGYGRRRRRSLPEAGPGR 158
             |:|                  ||  ||||||||  ||||
Db  146  LCHKFYLQGRCPYGSRCHFIHNPSEDLAAPGHPPVLRQSISFSGLPSGRRTSPPPGLAG 205

Qy  159  TLVSSKPQAHGAPAPPSGSAP 179
             ||  |  |
Db  206  PSLSSSSFSPSSSPPPPGDLP 226
```

RESULT 6
KFHU5
coagulation factor V precursor [validated] - human
N;Alternate names: coagulation labile factor; proaccelerin
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000
C;Accession: A56172; A42344; A28028; A27498; A25897
R;Cripe, L.D.; Moore, K.D.; Kane, W.H.
Biochemistry 31, 3777-3785, 1992
A;Title: Structure of the gene for human coagulation factor V.
A;Reference number: A42344; MUID:92232668
A;Accession: A56172
A;Molecule type: DNA
A;Residues: 1-2224 <CRI>
A;Cross-references: GB:J05368
A;Accession: A42344
A;Molecule type: DNA
A;Residues: 48-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
2070;2111-2120;2172-2181 <CR2>
R;Jenny, R.J.; Pittman, D.D.; Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kaufm
Proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987
A;Title: Complete cDNA and derived amino acid sequence of human factor V.
A;Reference number: A28028; MUID:87260886
A;Accession: A28028
A;Molecule type: mRNA
A;Residues: 1-857,'R',859-864,'R',866-924,'E',926-1763,'I',1765-2212,'T',2214-2224 <JEN>
A;Cross-references: GB:M16967
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Biochemistry 26, 6508-6514, 1987
A;Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hum
A;Reference number: A27498; MUID:88107560
A;Accession: A27498
A;Molecule type: mRNA
A;Residues: 1-1284,'I',1286-1600 <KAN>
A;Cross-references: GB:M17785
A;Note: parts of this sequence were determined by protein sequencing
R;Kane, W.H.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 6800-6804, 1986
A;Title: Cloning of a cDNA coding for human factor V, a blood coagulation factor homolog
A;Reference number: A25897; MUID:86313665
A;Accession: A25897
A;Molecule type: mRNA
A;Residues: 1188-1215,1315-2224 <KA2>
A;Cross-references: GB:M14335
A;Note: parts of this sequence were determined by protein sequencing
R;Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
Biochemistry 34, 4118-4124, 1995
A;Title: Thrombin-catalyzed activation of recombinant human factor V.
A;Reference number: A56139; MUID:95210278
A;Contents: annotation: thrombin cleavage sites

C;Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
C;Genetics:
A;Gene: GDB:F5
A;Cross-references: GDB:119896; OMIM:227400
A;Map position: 1q23-1q23
C;Function:
A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1;
A;Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa p
A;Pathway: blood coagulation
C;Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase
C;Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasm
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-2224/Product: coagulation factor V #status predicted <MAT>
F;29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
F;29-345/Domain: A1 <DA1>
F;33-329/Domain: ferroxidase repeat homology <FO1>
F;346-691/Domain: A2 <DA2>
F;351-684/Domain: ferroxidase repeat homology <FO2>
F;692-1573/Domain: B <DOB>
F;1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F;1574-2224/Product: coagulation factor Va light chain #status experimental <VAL>
F;1574-1905/Domain: A3 <DA3>
F;1581-1905/Domain: ferroxidase repeat homology <FO3>
F;1667-1765/Region: phospholipid binding #status predicted
F;1906-2064/Domain: C1 <DC1>
F;1906-2061/Domain: discoidin I amino-terminal homology <DN1>
F;2065-2224/Domain: C2 <DC2>
F;2065-2221/Domain: discoidin I amino-terminal homology <DN2>
F;51,55,239,297,460,468,554,741,752,760,776,782,821,938,977,1074,1083,1103,1106,1479,
F;167-193,248-329,500-526,603-684,1725-1751,1907-2061,2066-2221/Disulfide bonds: #sta
F;334-335/Cleavage site: Arg-Asn (protein C) #status predicted
F;363,693,1546/Binding site: sulfate (Tyr) (covalent) #status predicted
F;376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
F;382,1338/Binding site: carbohydrate (Asn) (covalent) #status absent
F;534-535/Cleavage site: Arg-Gly (protein C) #status predicted
F;737-738/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment
F;1046-1047/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experime
F;1573-1574/Cleavage site: Arg-Ser (thrombin) #status experimental <VAL>
```

```
Query Match    9.4%;  Score 89;  DB 1;  Length 2224;
Best Local Similarity  23.2%;  Pred. No. 10;
Matches  39;  Conservative  26;  Mismatches  71;  Indels  32;  Gaps  5;

Qy    3  VALMYLGSLAFLGADTAR------------LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD  55
             : ::|  |:|                         ::  |  ||:
Db  847  IRLLSLGAGEFKSQEHAKHKGPKVERDQAAKHRFSWMKLLAHKVGRHLSQDTGPSPSGMRP 906

Qy   56  VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT 111
             | |                    :::|:|              :::
Db  907  WEDLPSQDTGPSRMRPWKDPPSDLLLKQSNSSKILVGRWHLAS----------- 951

Qy  112  CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-PGR 158
             | ::: |  :|  ||   |  || ||| |:|       ||
Db  952  ---EKGSYEIIQ--DTDEDTAVNNWLISPQNASRAWGESTPLANKPGK 994
```

RESULT 7
T52311
isopenicillin N epimerase [validated] - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52311
R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
J. Bacteriol. 172, 3952-3958, 1990
A;Title: The beta-lactam biosynthetis genes for isopenicillin N epimerase and deaceto
A;Reference number: 226033; MUID:90299822
A;Accession: T52311
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 <KOV>
A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
C;Genetics:
A;Gene: cefD

Query Match   9.3%; Score 88.5; DB 2; Length 398;
Best Local Similarity 24.7%; Pred. No. 1.7;
Matches 46; Conservative 20; Mismatches 63; Indels 57; Gaps 11;

Qy   13 FLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQ-TLIRPQDMK 71
         ||||||||||||||| ||:||||||| : ||| ||||||:||:|
Db 198 FLDLDLSRIP-CDFYAGSGHKWLLA----------PTGVGFLHLAPGRLEELEPTQVS 244

Qy   72 GASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT------CTVQKLAHQIYQF 124
         |: :| | |||:|||:||||||||| || ||||||||||
Db 245 WAYEPPEGSGPPAARDR------FGSTPGLRRLECE-GTRDICPWLATPESIDFQ---- 292

Qy 125 TDKDKDNVAPRSKISPQGYGRRRRRSLPEAG PGRTLVS-SKPQAHGAPA---- 172
          ::: ||| :|: | |:|| || |: ||| :|| :|:||||
Db 293 --------AELGP-GAIRARRRELTDHARRLLADRPGRTLLTPDSPELSGGMVAYRL 340

Qy 173 PPSGSA 178
         || |
Db 341 PPGTDA 346

RESULT 8
I49481
alpha-2 adrenergic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49481
R;Link, R.; Daunt, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
A;Title: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and id
in antagonist binding.
A;Reference number: I49480; MUID:92342131
A;Accession: I49481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-450 <RES>
A;Cross-references: GB:M99377; NID:g191882; PIDN:AAA37213.1; PID:g191883
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match   9.2%; Score 87; DB 2; Length 450;
Best Local Similarity 28.9%; Pred. No. 2.7;
Matches 35; Conservative 14; Mismatches 54; Indels 18; Gaps 6;

Qy   69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
         |: ||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db 173 EKKGAGGGQPAEPSCKINDQKWYVIS------SSIGSFFAPCLIMILVYVRIYQIA-K 224

Qy 128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
         ||| || | |:| :|| |:||:| ||:|
Db 225 RRTRVPPSRRGPDACSAPPGGADRRPNGLGPERGAGPTGAEAEPLPTQLNGAPGEPAPAG 284

Qy 179 P 179
         |
Db 285 P 285

RESULT 9
A41870
dnaA protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 02-Feb-2001
C;Accession: A41870
R;Calcutt, M.J.; Schmidt, F.J.
J. Bacteriol. 174, 3220-3226, 1992
A;Title: Conserved gene arrangement in the origin region of the Streptomyces coelicolor
A;Reference number: A41870; MUID:92250416
A;Accession: A41870
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:M82836; NID:g6539740; PIDN:AAA26734.1; PID:g153240

R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: 221575
A;Accession: T36566
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <OLI>
A;Cross-references: EMBL:AL049826; PIDN:CAB42692.1; GSPDB:GN00070; SCOEDB:SCH24.01c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: dnaA; SCOEDB:SCH24.01c
A;Start codon: GTG
C;Keywords: DNA binding; nucleotide binding; P-loop
F;357-364/Region: nucleotide-binding motif A (P-loop)
F;416-420/Region: nucleotide-binding motif B

Query Match   9.2%; Score 87; DB 2; Length 656;
Best Local Similarity 25.4%; Pred. No. 4;
Matches 43; Conservative 16; Mismatches 64; Indels 46; Gaps 6;

Qy   14 LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA 73
         | |||| || :|| | |:|||| ||||||||||:||| |: |:||||| : |
Db   44 LVADTALLAVPNEFAK----GVLEGRLAPIVSETLSRECGRPIRIAITVDDTAGE 94

Qy   74 SRSPEDSSPDAARIRVK-RYRQS--MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD 130
         : : | || :| ||:| || | :| | | EYRDRDE- 135
Db   95 PAGPAPQAPQSPPSRPQHRYEPPELAPAPGQGRE-----------EYRDRDE- 135

Qy 131 NVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP 179
          |: :| :| :|| | |:|: :||:|
Db 136 --------YEGYGRNRADQLPTARP------AYPQEYQRPEPGSWPRP 169

RESULT 10
T29586
hypothetical protein F55F8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29586
R;Gattung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55F8.
A;Reference number: 220647
A;Accession: T29586
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-560 <GAT>
A;Cross-references: EMBL:U80447; PIDN:AAB37808.1; GSPDB:GN00019; CESP:F55F8.4
A;Experimental source: strain Bristol N2; clone F55F8
C;Genetics:
A;Gene: CESP:F55F8.4
A;Map position: 1
A;Introns: 56/2; 153/1; 320/1

Query Match   8.8%; Score 83.5; DB 2; Length 560;
Best Local Similarity 21.4%; Pred. No. 7.1;
Matches 37; Conservative 22; Mismatches 77; Indels 37; Gaps 3;

Qy   22 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSS 81
         :|: ||| | |: ||||||:||||||||||||||| |:|||| : | ||:||||
Db 372 EVRSSERKRSRRDDSPNAKRSIGLKSPERRSSRDRKSSPKQRQDSPVRRR---RSPSSIR 428

Qy   82 PDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDN---------- 131
         || :| ||: || | ||| | |:|:
Db 429 KESQRVRKHSPEQKRNGRHDSRS-------------VSPVRRRRRSPSPDNRQLGSRKQYS 475

Qy 132 --------VAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
             ||| |:| | :|| | |:|:   :||:|
Db 476 PLRRRQSSPMVASPRRRRRSPSPERQKRKRRSPSDSPPTRRLSTSPIRRRRSPSP 528

RESULT 11
I66868

cdc25B - rat
C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 22-Jun-1999
C;Accession: I66868
R;Jinno, S.; Suto, K.; Nagata, A.; Igarashi, M.; Kanaoka, Y.; Nojima, H.; Okayama, H.
EMBO J. 13, 1549-1556, 1994
A;Title: Cdc25A is a novel phosphatase functioning early in the cell cycle.
A;Reference number: 153194; MUID:94208523
A;Accession: I66868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-574 <RES>
A;Cross-references: GB:D16237; NID:g484292; PIDN:BAA03762.1; PID:g1008042
C;Superfamily: human protein-tyrosine-phosphatase cdc25A; cdc25-type protein-tyrosine-ph
C;Superfamily: cdc25-type protein-tyrosine-phosphatase homology <PTP>
F;366-556/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTP>

```
Query Match             8.8%;  Score 83.5; DB 2;  Length 574;
Best Local Similarity  23.3%;  Pred. No. 7.3;
Matches    47;  Conservative   23;  Mismatches   79;  Indels   53;  Gaps    7;

Qy      6 MYLGSLAFLGADTARLDVAS-EFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTL 64
          || :||  ||::||  |    :  :||| |  ::| |   ||:|:|
Db     59 MY--NLAGLGSEFPKTQVGSLSFQNRLTDLSLSRRTSECSLSSE---SSESSDAGLCMDS 113

Qy     65 IRPQDMKGASRSPEDSSPDAARIRVKR--------------------YRQSMNNFQGLRSFG 106
          ||                                            :|
Db    114 PSPMDPQTAERTFEQAIQAASRVIQKMQFTIKASVFASEAAGHSPVLQNITNSQALDSW- 172

Qy    107 CRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISP------QGYGRRRRRSLPEAGPGRTL 160
              :|  |  ||  |          ::  ||  :  |
Db    173 -------EKDEAGYRAASSPGEDKENDGYIFKMPQKLPHSSSARAL 211

Qy    161 VSSKPQAHGAPAPPSGSAPHFL 182
          ||  ::| |||
Db    212 AEWASRREAFTQRPS-SAPDLM 232
```

RESULT 12
C95367
conserved hypothetical protein SMa1548 [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: C95367
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meillot
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Accession: C95367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1051 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65501.1; PID:g14523974; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
  L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Contents: annotation
C;Genetics:
A;Gene: SMa1548
A;Genome: plasmid

```
Query Match             8.8%;  Score 83; DB 2;  Length 1051;
Best Local Similarity  26.9%;  Pred. No. 16;
Matches    46;  Conservative   18;  Mismatches   91;  Indels   16;  Gaps    7;

Qy     13 FLGADTARLDVASEFRKK-----WNKWALSRGKRELRMSSS---YPTGLADVKAGPAQTL 64
```

Db   310 FFRATAGKEPVRSEYRLRRADGSW-AWVIDVGQPRFSADGTFLGYVGSVLDITERRAAE- 367
Qy   65 IRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQF 124
Db   368 IAQQEAQAFIRSIFDSSPDCVRVLDMEGRPLLMNEAGRRIFGLNEGAPVTGQTWDSIGRA 427
Qy   125 TDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTL--VSSKP-QAHGAP 171
Db   428 SDADKVEAAWES--VRRGKTARFEISVRDAGGEERCMDVISAPITDHHGKP 476

RESULT 13
JH0190
alpha-2-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C;Accession: JH0190
R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Biochem. 97, 161-172, 1990
A;Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic recepto
A;Reference number: JH0190; MUID:91125329
A;Accession: JH0190
A;Molecule type: mRNA
A;Residues: 1-450 <CHA>
A;Experimental source: brain
C;Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It me
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;34-59/Domain: hydrophobic <HDI>
F;71-96/Domain: hydrophobic <HII>
F;106-131/Domain: hydrophobic <III>
F;150-175/Domain: hydrophobic <HIV>
F;193-218/Domain: hydrophobic <HDV>
F;375-400/Domain: hydrophobic <HVI>
F;405-430/Domain: hydrophobic <VII>

```
Query Match             8.7%;  Score 82.5; DB 2;  Length 450;
Best Local Similarity  25.5%;  Pred. No. 6.9;
Matches    40;  Conservative   23;  Mismatches   73;  Indels   21;  Gaps    7;

Qy     33 KWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRY 92
          :  |  : ||  | :: :|| :|             || ::|||| : :|  :
Db    140 EYNLKRTRRRIKAIHCHCVVISAVISFFPLISI---EKKGAGGGQQPAEPSCKINDQKWY 196

Qy     93 RQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDKDKDNVAPRSK-----ISPQGYGRR 146
          : :     |   |         |: || :|:|     ::  :           ||:|  |
Db    197 VIS------SSIGSFFAPCLIMLVVRIYQIA-KRRTRVPPSRRGPDACSAPPGGADR 248

Qy    147 RRRSL-PEAGPGRTLVSSKP--QAHGAPAPPSGSAP 179
          |  :| ||  |          :  ::|  |
Db    249 RPNGLGPERGAGTAGGEAEPLPTQLNGAPGEPAPTRP 285
```

RESULT 14
F88632
protein F56B3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88632
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: F88632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-926 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC02615.1; PID:g2854201; GSPDB:GN00022; CESP:F56
C;Genetics:
A;Gene: F56B3.4
A;Map position: 4

```
Query Match              8.6%;   Score 81.5;  DB 2;  Length 926;
Best Local Similarity   24.0%;   Pred. No. 19;
Matches  29;  Conservative  19;  Mismatches  64;  Indels  9;  Gaps  3;

Qy      7 YLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIR 66
            || ||| :||:: :|: :||:  |  |  |:: || |
Db    542 YLKSLDFEKIQEMKLEITERFDPKLLEFLKNRGNKASETQKKPKKISKFKASRQQK--E 599

Qy     67 PQ-DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFT 125
           |: :||| | :|| | :| |: || |:|||  :|| |:    :: ::
Db    600 PENEQKGAPEPPAQAPP-----TKVVEEMMNELEVLEEYGNREDQEKYNRLATVFWKII 653

Qy    126 D 126
            |
Db    654 D 654


RESULT 15
B40392
alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C;Accession: B40392
R;Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A;Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec
A;Reference number: A40392; MUID:91244823
A;Accession: B40392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <LAN>
A;Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match              8.6%;   Score 81;  DB 2;  Length 450;
Best Local Similarity   27.3%;   Pred. No. 9.5;
Matches  33;  Conservative  13;  Mismatches  57;  Indels  18;  Gaps  5;

Qy     69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
           : ||| :: ||  |  | |  |||||||||||||||| ||:|||| :|||| |:||:|| |
Db    173 EKKGAGGGQQPAEPSCKINDQKWYIS------SSIGSFFAPCLIMILVYVRIYQIA-K 224

Qy    128 DKDNVAPRSK------ISPQGYGRRRRRSLPEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
           :| | |:: |     |  |  :| : ||| |: ||| |: :| |:
Db    225 RRTRVPPSRRGPDACSAPPGGADRRPNAVGPERGAGTAGAEAEPLPTQLNGAPGEPAPTR 284

Qy    179 P 179
            |
Db    285 P 285


Search completed: October 17, 2002, 15:22:41
Job time : 18.1922 secs
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                    GenCore version 5.1.3
             Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       October 17, 2002, 15:20:12 ; Search time 31.4202 Seconds
                                           (without alignments)
                                           643.390 Million cell updates/sec

Title:        US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence:     1 VSVALMYLGSLAFLGADTAR.........SKPQAHGAPAPPSGSAPHFL 182

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:        747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    A_Geneseq_032802:*
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           2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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           4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
           5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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           7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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          11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
          12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
          13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
          14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
          15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
          16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
          17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
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          19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
          20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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          22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	947	100.0	185	22	AAB49697	Human adrenomedulli
2	947	100.0	185	22	AAB60344	Human adrenomedulli
3	817	86.3	188	22	AAB49698	Porcine adrenomedu
4	817	86.3	188	22	AAB60345	Porcine adrenomedu
5	624.5	65.9	185	22	AAB49699	Rat adrenomedullin
6	624.5	65.9	185	22	AAB60346	Rat adrenomedullin
7	469	49.5	97	21	AAG00251	Human secreted pro
8	305.5	32.3	120	22	AAB75122	UspA(1-57)-(A)-(GS
9	298	31.5	147	22	AAB75124	UspA(1-84)-(A)-(GS
10	297.5	31.4	120	22	AAB75123	UspA(1-56)-(DD)-(G
11	289	30.5	53	22	AAB75111	Glycine extended h

12	289	30.5	53	22	AAB75112	Glycine extended a
13	289	30.5	62	22	AAB75113	Linker peptide-adr
14	289	30.5	170	22	AAB75114	Thioredoxin-(GSGSG
15	283	29.9	52	22	AAB75110	Human adrenomedull
16	283	29.9	52	22	AAB91759	Adrenomedullin pep
17	283	29.9	52	22	AAE09818	Human adrenomedull
18	239	25.2	48	22	AAB91763	Adrenomedullin pep
19	231	24.4	50	22	AAE09819	Rat adrenomedullin
20	227	24.0	52	22	AAB91765	Adrenomedullin pep
21	219.5	23.2	53	22	AAB91767	Adrenomedullin pep
22	196	20.7	40	22	AAB91768	Adrenomedullin pep
23	181.5	19.2	37	22	AAB91761	Adrenomedullin pep
24	176	18.6	33	22	AAB91764	Adrenomedullin pep
25	163	17.2	31	18	AAW25160	Human preproadreno
26	163	17.2	31	22	AAB91762	Adrenomedullin pep
27	163	17.2	31	22	AAE09827	Human adrenomedull
28	107	11.3	31	22	AAW25161	Human proadrenomed
29	104	11.0	20	22	AAB91766	Adrenomedullin pep
30	97	10.2	20	22	AAB91769	Adrenomedullin pep
31	89.5	9.5	326	22	AAB71705	Human TTP protein.
32	89	9.4	2224	17	AAW04254	Human Factor V. H
33	89	9.4	2224	20	AAY49564	Human lipoprotein
34	88.5	9.3	926	19	AAW44883	Chimeric polyproli
35	87.5	9.2	177	22	AAB63878	Human prostate can
36	86.5	9.1	500	16	AAR72590	Acremonium chrysog
37	86.5	9.1	654	20	AAY26901	Amphotrophic MLV r
38	85	8.7	647	20	AAY26907	Amphotrophic MLV r
39	82	8.7	145	22	ABG05153	Novel human diagno
40	81.5	8.6	167	19	AAW44910	"polyproline beta-
41	81.5	8.6	318	22	ABG19764	Novel human diagno
42	81.5	8.6	458	18	AAW26323	Murine leukaemia v
43	81.5	8.6	624	20	AAY26913	Envelope glycoprot
44	81.5	8.6	625	22	AAB19881	Murine leukemia vi
45	81.5	8.6	637	22	AAB19878	Murine leukemia vi

```
                         ALIGNMENTS

RESULT 1
AAB49697
ID   AAB49697 standard; Protein; 185 AA.
XX
AC   AAB49697;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; human.
XX
OS   Homo sapiens.
XX
PN   WO200078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999; 99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29138.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedullin -
XX
PS   Claim 1; Page 26-27; 42pp; Japanese.
```

```
XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedulin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the human adrenomedulin protein, which is used in the
CC   composition of the invention.
XX
SQ   Sequence 185 AA;

Query Match             100.0%;  Score 947;  DB 22;  Length 185;
Best Local Similarity   100.0%;  Pred. No. 2.1e-93;
Matches 182;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

Qy         61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy        121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy        181 FL 182
              ||
Db        184 FL 185

RESULT 2
AAB60344
ID   AAB60344 standard; Protein; 185 AA.
XX
AC   AAB60344;
XX
DT   06-APR-2001  (first entry)
XX
DE   Human adrenomedulin precursor.
XX
KW   Human; adrenomedulin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Homo sapiens.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999; 99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27228.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedulin -
XX
PS   Claim 7; Page 37-38; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedulin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedulin in

CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents human adrenomedulin precursor.
XX
SQ   Sequence 185 AA;

Query Match             100.0%;  Score 947;  DB 22;  Length 185;
Best Local Similarity   100.0%;  Pred. No. 2.1e-93;
Matches 182;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

Qy         61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy        121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 183

Qy        181 FL 182
              ||
Db        184 FL 185

RESULT 3
AAB49698
ID   AAB49698 standard; Protein; 188 AA.
XX
AC   AAB49698;
XX
DT   04-APR-2001  (first entry)
XX
DE   Porcine adrenomedulin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedulin; urinary disorder; incontinence; procine.
XX
OS   Sus scrofa.
XX
PN   WO200078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999;    99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29139.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedulin -
XX
PS   Disclosure; Page 31-33; 42pp; Japanese.
XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedulin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the porcine adrenomedulin protein, which is used in the
CC   composition of the invention.
XX
```

```
SQ   Sequence   188 AA;

Query Match             86.3%;  Score  817;  DB 22;  Length 188;
Best Local Similarity   89.1%;  Pred. No. 1.9e-79;
Matches  156;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy         1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
             | |||||||||||||||||:|:|||||||||||:|:|||||||||| ||||:|||:||||
Db         4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63

Qy        61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
             |||:||||| ||:: || : ||||||||||||||||||||||||||||||||||||||||
Db        64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy       121 IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
             |||||||||| ||||||||||||||||| ||||: ||| :||||||||||| :
Db       124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178

RESULT 4
AAB60345
ID   AAB60345 standard; Protein; 188 AA.
XX
AC   AAB60345;
XX
DT   06-APR-2001   (first entry)
XX
DE   Porcine adrenomedullin precursor.
XX
KW   Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Sus scrofa.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999;  99JP-0177548.
PR   21-MAR-2000;  2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27229.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin precursor.
XX
PS   Disclosure; Page 43-44; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents porcine adrenomedullin precursor.
XX
SQ   Sequence   188 AA;

Query Match             86.3%;  Score  817;  DB 22;  Length 188;
Best Local Similarity   89.1%;  Pred. No. 1.9e-79;
Matches  156;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy         1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
             | |||||||||||||||||:|:|||||||||||:|:|||||||||| ||||:|||:||||
Db         4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63

Qy        61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
             |||:||||| ||:: || : ||||||||||||||||||||||||||||||||||||||||
Db        64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123

Qy       121 IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
             |||||||||| ||||||||||||||||| ||||: ||| :||||||||||| :
Db       124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178

RESULT 5
AAB49699
ID   AAB49699 standard; Protein; 185 AA.
XX
AC   AAB49699;
XX
DT   04-APR-2001   (first entry)
XX
DE   Rat adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; rat.
XX
OS   Rattus norvegicus.
XX
PN   WO200078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999;  99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29140.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedullin -
XX
PS   Disclosure; Page 37-38; 42pp; Japanese.
XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the porcine adrenomedullin rat, which is used in the
CC   composition of the invention.
XX
SQ   Sequence   185 AA;

Query Match             65.9%;  Score  624.5;  DB 22;  Length 185;
Best Local Similarity   72.0%;  Pred. No. 8e-59;
Matches  126;  Conservative  14;  Mismatches  32;  Indels   3;  Gaps   2;

Qy         1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
             ||:|||:|||||:||||||||| ::||||||||||||||||||||:||||||||:||:||
Db         4 VSIALMLLGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP 63

Qy        61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
             :||| ||:  ::|:|:::||:|: || |||||||||||| :|| ::|||||||||:||||
Db        64 TQTL-GLQDKQSTSSTPQASTQSTAHIRVKRYRQSMN-QGSRSTGCRFGTCTMQKLAHQ 120

Qy       121 IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
             |||||||||| |||.||||||||||||| |||| : ||| :: | ::|:||:||
Db       121 IYQFTDKDKDGMAPRNKISPQGYGRRRRRSLPEVLRARTVESSQETHSAPASPA 175
```

```
RESULT 6
AAB60346
ID   AAB60346 standard; Protein; 185 AA.
XX
AC   AAB60346;
XX
DT   06-APR-2001  (first entry)
XX
DE   Rat adrenomedullin precursor.
XX
KW   Rat; adrenomedullin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Rattus norvegicus.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999;  99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27230.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Disclosure; Page 48-49; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents rat adrenomedullin precursor.
XX
SQ   Sequence  185 AA;

Query Match          65.9%;  Score 624.5;  DB 22;  Length 185;
Best Local Similarity  72.0%;  Pred. No. 8e-59;
Matches  126;  Conservative  14;  Mismatches  32;  Indels  3;  Gaps  2;

Qy     1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
         |:|||| |||| |||||||||| .:|:||||||||||||||||||| ||||||||||
Db     4 VSIALMLLGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP 63

Qy    61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
         ||||||||||||||||| :|::| || |||||||||||  ||  :|:::|||||||||||
Db    64 TQTL-GLQDKQSTSSTPQASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQ 120

Qy   121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKFQAHGAPAPPS 175
         |||||||||| :|| :|||||||||||||||||||  :|||||||:|||  :|||
Db   121 IYQFTDKDKDGMAPRNKISPQGYGRRRRRSLPEVLRARTVESSQEQTHSAPASPA 175
```

```
RESULT 7
AAG00251
ID   AAG00251 standard; Protein; 97 AA.
XX
AC   AAG00251;
XX
DT   06-OCT-2000  (first entry)
```

```
XX
DE   Human secreted protein, SEQ ID NO: 4332.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;  99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   N-PSDB; AAC00257.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 13; SEQ ID 4332; 71pp + CD-ROM; English.
XX
CC   The present sequence is a polypeptide encoded by one of a large number
CC   of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC   were prepared from total human RNAs or polyA+ RNAs derived from 30
CC   different tissues. EST sequences usually correspond mainly to the 3'
CC   untranslated region (UTR) of the mRNA because they are often obtained
CC   from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC   isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC   those cases where longer cDNA sequences have been obtained, the full 5'
CC   UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC   ends and can therefore be used to obtain full length cDNAs and genomic
CC   DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC   chromosome mapping procedures. They are used to obtain upstream
CC   regulatory sequences and to design expression and secretion vectors.
XX
SQ   Sequence  97 AA;

Query Match           49.5%;  Score 469;  DB 21;  Length 97;
Best Local Similarity 100.0%;  Pred. No. 1.6e-42;
Matches  93;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63

Qy    61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYR 93
         ||||||||||||||||||||||||||||||||
Db    64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYR 96
```

```
RESULT 8
AAB75122
ID   AAB75122 standard; Protein; 120 AA.
XX
AC   AAB75122;
XX
DT   31-JUL-2001  (first entry)
XX
DE   UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
```

```
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19864.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 68; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  120 AA;

Query Match           32.3%;     Score 305.5;  DB 22;   Length 120;
Best Local Similarity 65.0%;     Pred. No. 7.4e-25;
Matches  67; Conservative  3; Mismatches 12; Indels 21; Gaps  4;

Qy   42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
         ::  |-||||| |   ||  |: |             GSGDAF-----EYRQSMNNFQG 77
Db   39 DVNYSDLY-TGLIDVNLG------DMAGS------GSGDAF-----EYRQSMNNFQG 77

Qy  102 LRSFGCRFGTCTCVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
         ||||||||||||||||||||||||||||||||||||||||||||
Db   78 LRSFGCRFGTCTCVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 120

RESULT 9
AAB75124
ID   AAB75124 standard; Protein; 147 AA.
XX
AC   AAB75124;
XX
DT   31-JUL-2001  (first entry)
XX
DE   UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
```

```
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19866.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 71; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  147 AA;

Query Match           31.5%;     Score 298;  DB 22;   Length 147;
Best Local Similarity 57.4%;     Pred. No. 6.1e-24;
Matches  66; Conservative  6; Mismatches 25; Indels 18; Gaps  3;

Qy   42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS--------SPDAARIRV 89
         ::  |-|||  ||  |: |   :             ::   |  |
Db   39 DVNYSDLY-TGLIDVNLGDMQKRISEETHHALTELSTNAGYPITETLAGSGSGDAF---- 93

Qy   90 KRYRQSMNNFQGLRSFGCRFGTCTCVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 -EYRQSMNNFQGLRSFGCRFGTCTCVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 147

RESULT 10
AAB75123
ID   AAB75123 standard; Protein; 120 AA.
XX
AC   AAB75123;
XX
DT   31-JUL-2001  (first entry)
XX
DE   UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19865.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 69-70; 75pp; Japanese.
XX
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```
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   120 AA;

Query Match             31.4%;  Score 297.5;  DB 22;  Length 120;
Best Local Similarity   64.1%;  Pred. No. 5.3e-24;
Matches   66;  Conservative   3;  Mismatches 13;  Indels  21;  Gaps   4;

Qy   42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
         :: .||||||||  :  : |:    ||||||||
Db   39 DVNYSDLY-TGLIDVNLG--------DDDGS------GSGDAF-----EYRQSMNNFQG 77

Qy  102 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
         |||||||||||||||||||||||||||||||||||||||||
Db   78 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 120

RESULT 11
AAB75111
ID   AAB75111 standard; Protein; 53 AA.
XX
AC   AAB75111;
XX
DT   31-JUL-2001   (first entry)
XX
DE   Glycine extended human adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19807.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Example 1; Page 46; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   53 AA;


Query Match             30.5%;  Score 289;  DB 22;  Length 53;
Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
Matches   53;  Conservative   0;  Mismatches  0;  Indels   0;  Gaps   0;

Qy   92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 53

RESULT 12
AAB75112
ID   AAB75112 standard; Protein; 53 AA.
XX
AC   AAB75112;
XX
DT   31-JUL-2001   (first entry)
XX
DE   Glycine extended adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19808.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 47; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   53 AA;


Query Match             30.5%;  Score 289;  DB 22;  Length 53;
Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
Matches   53;  Conservative   0;  Mismatches  0;  Indels   0;  Gaps   0;

Qy   92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 53

RESULT 13
AAB75113
ID   AAB75113 standard; Protein; 62 AA.
XX
AC   AAB75113;
XX
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```
DT   31-JUL-2001  (first entry)
XX
DE   Linker peptide-adrenomedullin (AM) precursor protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A,  Mitsuda Y,  Nakayama T,  Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19809.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 20; Page 48; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   62 AA;

Query Match             30.5%;   Score 289;  DB 22;  Length 62;
Best Local Similarity   100.0%;  Pred. No. 1.8e-23;
Matches    53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 62

RESULT 14
AAB75114
ID   AAB75114 standard; Protein; 170 AA.
XX
AC   AAB75114;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Thioredoxin-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
```

```
XX
PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A,  Mitsuda Y,  Nakayama T,  Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19810.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 49-50; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   170 AA;

Query Match             30.5%;   Score 289;  DB 22;  Length 170;
Best Local Similarity   100.0%;  Pred. No. 6.8e-23;
Matches    53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 170

RESULT 15
AAB75110
ID   AAB75110 standard; Protein; 52 AA.
XX
AC   AAB75110;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Human adrenomedullin (AM) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A,  Mitsuda Y,  Nakayama T,  Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19806.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 45; 75pp; Japanese.
XX
```

```
CC    The present invention describes a method (M1) for producing
CC    adrenomedullin precursor. The method comprises: (a) producing the fused
CC    protein using a recombinant host cell; (b) restricted digestion of the
CC    fused protein by a protease followed by collection of sediment; and
CC    (c) dissolving the sediment and extracting adrenomedullin precursor.
CC    The method can be used for the production of adrenomedullin precursor
CC    for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC    and AAB75110 to AAB75124 represent sequences which are used in the
CC    exemplification of the present invention.
XX
SQ    Sequence    52 AA;

Query Match             29.9%;  Score 283;  DB 22;  Length 52;
Best Local Similarity   100.0%;  Pred. No. 6.4e-23;
Matches   52;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

Search completed: October 17, 2002, 15:21:13
Job time : 31.4202 secs
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```
                GenCore version 5.1.3
        Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   October 17, 2002, 15:20:12 ; Search time 6.51466 Seconds
                                       (without alignments)
                                       742.931 Million cell updates/sec

Title:          US-10-018-924-2_COPY_22_146
Perfect score:  655
Sequence:       1 ARLDVASEFRKKWNKWALSR........FTDKDKDNVAPRSKISPQGY 125

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:     105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	185	1	ADML_HUMAN	P35318 homo sapien
2	611	93.3	188	1	ADML_PIG	P53366 sus scrofa
3	606	92.5	188	1	ADML_BOVIN	Q62827 bos taurus
4	597	91.1	188	1	ADML_CANFA	O77559 canis famil
5	458.5	70.0	185	1	ADML_RAT	P43145 rattus norv
6	414	63.2	184	1	ADML_MOUSE	P97297 mus musculu
7	77	11.8	591	1	PTRR_MOUSE	P41593 mus musculu
8	75	11.5	591	1	PTRR_RAT	P25961 rattus norv
9	71.5	10.9	477	1	FIBB_PETMA	P02678 petromyzon
10	71	10.8	2224	1	FA5_HUMAN	P12259 homo sapien
11	69	10.5	454	1	PRI1_SCHPO	O14215 schizosacch
12	68.5	10.5	479	1	FIBB_RAT	P14480 rattus norv
13	68.5	10.5	3144	1	VP13_YEAST	Q07878 saccharomyc
14	67.5	10.3	300	1	MOXJ_METEX	P16028 methylobact
15	67	10.2	436	1	SLS6_BRAOL	P07761 brassica ol
16	67	10.2	457	1	TBA_DICDI	P32255 dictyosteli
17	66	10.1	380	1	GBB_MAIZE	P49178 zea mays (m
18	66	10.1	397	1	SKI8_YEAST	Q02793 saccharomyc
19	65.5	10.0	400	1	GUN5_BACAG	O85465 bacillus ag
20	65.5	10.0	448	1	TBAA_SCHCO	Q49741 schizophyll
21	65.5	10.0	451	1	TBA2_EMENI	P24634 emericella
22	65.5	10.0	497	1	SC14_YARLI	P45816 yarrowia li
23	65.5	10.0	532	1	TYRO_RANNI	Q04604 rana nigrom
24	65	9.9	442	1	TOP5_BPT4	P07065 bacteriopha
25	65	9.9	485	1	GLR_RAT	P30082 rattus norv
26	65	9.9	573	1	EYA3_HUMAN	Q99504 homo sapien
27	65	9.9	1252	1	RPOB_CHLMU	P56869 chlamydia m
28	65	9.9	1252	1	RPOB_CHLTR	O84317 chlamydia t
29	65	9.9	3210	1	CENF_HUMAN	P49454 homo sapien
30	64.5	9.8	409	1	GUN2_BACS4	P06565 bacillus sp
31	64.5	9.8	491	1	FIBB_HUMAN	P02675 homo sapien
32	64.5	9.8	905	1	YD83_HUMAN	Q9P2Q4 homo sapien
33	63.5	9.7	397	1	CEFD_STRCL	P18549 streptomyce
34	63.5	9.7	458	1	A2AC_MOUSE	Q01337 mus musculu
35	63.5	9.7	458	1	A2AC_RAT	P22086 rattus norv
36	63.5	9.7	477	1	GLR_HUMAN	P47871 homo sapien
37	63.5	9.7	677	1	SPOT_HAEIN	P43811 haemophilus
38	63.5	9.7	980	1	SYN_DROME	Q24546 drosophila
39	63	9.6	215	1	Y457_ANASP	P29713 anabaena sp
40	63	9.6	440	1	GAT4_MOUSE	Q08369 mus musculu
41	63	9.6	459	1	G33_RAT	P05432 rattus norv
42	63	9.6	463	1	FIBB_CHICK	Q02020 gallus gall
43	63	9.6	995	1	DBPA_YEAST	Q12389 saccharomyc
44	62.5	9.5	108	1	SVS4_MOUSE	P18419 mus musculu
45	62.5	9.5	360	1	VP3_ARMV	P24820 arabis mosa

```
                              ALIGNMENTS

RESULT 1
ADML_HUMAN
ID   ADML_HUMAN     STANDARD;      PRT;   185 AA.
AC   P35318;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93343928; PubMed=7688224;
RA   Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT   "Cloning and characterization of cDNA encoding a precursor for human
RT   adrenomedullin.";
RL   Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94354869; PubMed=8074714;
RA   Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA   Kitamura K., Eto T., Matsuo H.;
RT   "Genomic structure of human adrenomedullin gene.";
RL   Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN   [3]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [4]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445;
RA   Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
CC       PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
CC       KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
```

```
CC   INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC   PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC   INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC   AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
CC   ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC   VESSELS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
CC       ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC       TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JN0476; JN0476.
DR   PIR; JN0684; JN0684.
DR   PIR; JC2351; JC2351.
DR   MIM; 103275; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    185       PREPROAM C-TERMINAL FRAGMENT.
FT   DISULFID    110    115
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

Query Match             100.0%;  Score 655; DB 1;  Length 185;
Best Local Similarity   100.0%;        Pred. No. 1e-61;
Matches  125;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81

Qy     61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141

Qy    121 SPQGY 125
          |||||
Db    142 SPQGY 146

RESULT 2
ADML_PIG
ID   ADML_PIG      STANDARD;     PRT;    188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning
RT   of cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]
RP   SEQUENCE OF 22-41.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin
RT   N-terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC       KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D14875; BAA03590.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      153    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   188 AA;  20893 MW;  71749460F5660A61 CRC64;

Query Match             93.3%;  Score 611; DB 1;  Length 188;
Best Local Similarity   91.2%;        Pred. No. 4.4e-57;
Matches  114;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
          ||||||||:||||||||||||||||||||||:||||||||||:||||||||:|||||||||
Db     22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81

Qy     61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
          ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db     82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141

Qy    121 SPQGY 125
          |||||
Db    142 SPQGY 146

RESULT 3
ADML_BOVIN
ID   ADML_BOVIN    STANDARD;     PRT;    188 AA.
AC   062827;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
```

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GN   ADM.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC       CIRCULATION CONTROL (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
SQ   SEQUENCE   188 AA;  20981 MW;  3002E79AB3B6612C CRC64;

Query Match             92.5%;  Score 606;  DB 1;  Length 188;
Best Local Similarity   92.0%;  Pred. No. 1.5e-56;
Matches  115;  Conservative   4;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
          ||||||||||||||||||||||||||:|||||||||||||||:|||||||||||||||
Db   22 ARLDVAAEFRKKWNKWALSRGKRELRESSSYPTGLADVKAGPVQTLIRPQDVKGASRSPQ 81

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
          |||||||||||||||||||:|||||||||||||||||||||||| ||||| |||||||
Db   82 ASSPDAARIRVKRYRQSLNNFQGLRSFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKI 141

Qy  121 SPQGY 125
          |||||
Db  142 SPQGY 146

RESULT 4
ADML_CANFA
ID   ADML_CANFA    STANDARD;    PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
```

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OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99902704; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF045773; AAD05423.1; -.
DR   EMBL; U96127; AAD09957.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   CONFLICT    130    130       N -> K (IN REF. 2).
SQ   SEQUENCE   188 AA;  20929 MW;  809D6A64F9BF5578 CRC64;

Query Match             91.1%;  Score 597;  DB 1;  Length 188;
Best Local Similarity   90.4%;  Pred. No. 1.3e-55;
Matches  113;  Conservative   6;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
          |||||||||||||||||:||||||||:|||||||||::|||||||||:||||||||||::
Db   22 ARLDVASEFRKKWNKWAVSRGKRELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQ 81

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
          :|||||||||||||||||||||:|||||||||||||||||||||||||:|| ||||||||
Db   82 TSGPDAARIRVKRYRQSMNNFQGPRSFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKI 141

Qy  121 SPQGY 125
          |||||
Db  142 SPQGY 146

RESULT 5
ADML_RAT
ID   ADML_RAT    STANDARD;    PRT;   185 AA.
AC   P43145;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
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OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX   MEDLINE=93388621; PubMed=7690563;
RA   Sakata J., Shimokubo T., Kitamura K., Nakamura S., Kangawa K.,
RA   Matsuo H., Eto T.;
RT   "Molecular cloning and biological activities of rat adrenomedullin, a
RT   hypotensive peptide.";
RL   Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96102137; PubMed=8524787;
RA   Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA   Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT   "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT   its role in exacerbating focal brain ischemic damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC       HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     91       BY SIMILARITY.
FT   PEPTIDE      94    143       ADRENOMEDULLIN.
FT   PROPEP      149    185       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    107    112       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     143    143       AMIDATION (G-144 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
SQ   SEQUENCE   185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;

Query Match             70.0%;  Score 458.5;  DB 1;  Length 185;
Best Local Similarity   72.8%;  Pred. No. 4.3e-41;
Matches   91;  Conservative   10;  Mismatches   21;  Indels    3;  Gaps    2;

Qy     1  ARLDVASEFRKKWNKWALSRGKRELRMSSSYYPTGLADVKAGPAQTLIRPQDMKGASRSPE  60
          ||||| :|:||||||||||||||||||||| ::|||:||||||||||||||| :: ::||
Db    22  ARLDTSSQFRKKWNKWALSRGKRELQASSSYYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ  80

Qy    61  DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI  120
          |: :||||||||||||||| | |||||||||||||||||||||||||||:||| :||||
Db    81  ASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKI  138

Qy   121  SPQGY  125
          |||||
Db   139  SPQGY  143
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RESULT 6
ADML_MOUSE
ID   ADML_MOUSE     STANDARD;     PRT;    184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RA   Yotsumoto S., Ko M.S.H.;
RT   "Expression of mouse adrenomedullin gene in trophoblastic giant
RT   cells at the implantation site.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    144       ADRENOMEDULLIN.
FT   PROPEP      151    184       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    108    113       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     144    144       AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   CONFLICT    173    173       A -> G (IN REF. 2).
SQ   SEQUENCE   184 AA;  20764 MW;  C88C99045A79C898 CRC64;

Query Match             63.2%;  Score 414;  DB 1;  Length 184;
Best Local Similarity   68.9%;  Pred. No. 2e-36;
Matches   84;  Conservative    8;  Mismatches   28;  Indels    2;  Gaps    1;

Qy     4  DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSS   63
          | :||||||||||||||||||||||| |||||||||:: :: ||: ||
Db    25  DTPSQFRKKWNKWALSRGKRELQASSSYPTGLADETTVPTQTLDPFLDEQNTTGPLQASN   84

Qy    64  PDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQ  123
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Db      85 QSEAHIRVKRYRQSMN--QGSRSNGCRFGTCTFQKLAHQIYQLTDKDKDGMAPRNKISPQ 142
            | ||||||||||||  ||  ||  || |||||||| |||||||||| ||||||  :||:||||
Qy     124 GY 125
            ||
Db     143 GY 144
```

RESULT 7

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PTRR_MOUSE
ID   PTRR_MOUSE    STANDARD;    PRT;    591 AA.
AC   P41593; Q62119;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone/parathyroid hormone-related peptide receptor
DE   precursor (PTH/PTHR receptor).
GN   PTHR1 OR PTHR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/HEHA;
RX   MEDLINE=95034305; PubMed=7524627;
RA   McCuaig K.A., Clarke J.C., White J.H.;
RT   "Molecular cloning of the gene encoding the mouse parathyroid
RT   hormone/parathyroid hormone-related peptide receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=94255468; PubMed=8197183;
RA   Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,
RA   Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT   "Expression pattern of parathyroid hormone/parathyroid hormone
RT   related peptide receptor mRNA in mouse postimplantation embryos
RT   indicates involvement in multiple developmental processes.";
RL   Mech. Dev. 47:29-42(1994).
CC   -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC       PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC       RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC       CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC       SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X78936; CAA55536.1; -.
DR   EMBL; L34611; AAA40011.1; -.
DR   EMBL; L34608; AAA40011.1; JOINED.
DR   EMBL; L34607; AAA40011.1; JOINED.
DR   EMBL; L34609; AAA40011.1; JOINED.
DR   EMBL; L34610; AAA40011.1; JOINED.
DR   HSSP; Q03431; 1BL1.
DR   GCRDb; GCR_1005; -.
DR   GCRDb; GCR_1614; -.
DR   MGD; MGI:97801; Pthr.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR001879; hormn_receptor.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF02793; HRM; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00008; HormR; 1.
DR   PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR   PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    591       PARATHYROID HORMONE/PARATHYROID HORMONE-
FT                                RELATED PEPTIDE RECEPTOR.
FT   DOMAIN       27    188       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    189    212       1 (POTENTIAL).
FT   DOMAIN      214    219       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    220    239       2 (POTENTIAL).
FT   DOMAIN      240    282       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    283    306       3 (POTENTIAL).
FT   DOMAIN      307    320       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    321    342       4 (POTENTIAL).
FT   DOMAIN      343    361       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    362    382       5 (POTENTIAL).
FT   DOMAIN      383    409       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    410    428       6 (POTENTIAL).
FT   DOMAIN      429    440       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    441    463       7 (POTENTIAL).
FT   DOMAIN      464    591       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    176    176       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     27     28       DA -> TS (IN REF. 2).
FT   CONFLICT    464    465       MISSING (IN REF. 2).
FT   CONFLICT    500    501       GA -> VS (IN REF. 2).
SQ   SEQUENCE   591 AA;  66313 MW;  F7876F8D388BDDFD CRC64;

Query Match             11.8%;  Score 77;  DB 1;  Length 591;
Best Local Similarity   32.5%;  Pred. No. 1.6;
Matches   26;  Conservative   12;  Mismatches   28;  Indels   14;  Gaps    5;

Qy       4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP------TGLADV-KAG---PAQTLIRP 49
           :|:||:|||:||:|| :||: |||:  ::|:   |:||    :|| |:|   :|
Db     465 EVQAEIRKSWSRWTLALDFKRKARSGSSSYGPMGAHTSVTNVGPRAGLSLPLSPRLLP 524

Qy      50 QDMKGASRSPEDSSPDAARI 69
           | |:| | | |||    | |
Db     525 ATTNGHSQLPGHAKPGAPAI 544
```

RESULT 8

```
PTRR_RAT
ID   PTRR_RAT      STANDARD;    PRT;    591 AA.
AC   P25961;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Parathyroid hormone/parathyroid hormone-related peptide receptor
DE   precursor (PTH/PTHR receptor).
GN   PTHR1 OR PTHR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone;
RX   MEDLINE=92212903; PubMed=1313566;
RA   Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
RA   Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
RA   Kronenberg H.M., Segre G.V.;
RT   "Expression cloning of a common receptor for parathyroid hormone and
RT   parathyroid hormone-related peptide from rat osteoblast-like cells: a
RT   single receptor stimulates intracellular accumulation of both cAMP
RT   and inositol trisphosphates and increases intracellular free
RT   calcium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=94292182; PubMed=8020952;
RA   Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,
RA   Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
RT   "Cloning of a parathyroid hormone/parathyroid hormone-related peptide
RT   receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) cell line:
RT   chromosomal assignment of the gene in the human, mouse, and rat
RT   genomes.";
RL   Genomics 20:20-26(1994).
CC   -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC       PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC       RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC       CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC       SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; M77184; AAA41811.1; -.
DR   EMBL; L19475; AAA68098.1; -.
DR   HSSP; Q03431; 1BL1.
DR   GCRDb; GCR_0206; -.
DR   GCRDb; GCR_0938; -.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR001879; hormn_receptor.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF02793; HRM; 1.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00008; HormR; 1.
DR   PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR   PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    591       PARATHYROID HORMONE/PARATHYROID HORMONE-
FT                                RELATED PEPTIDE RECEPTOR.
FT   DOMAIN       27    188       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    189    212       1 (POTENTIAL).
FT   DOMAIN      213    219       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    220    239       2 (POTENTIAL).
FT   DOMAIN      240    282       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    283    306       3 (POTENTIAL).
FT   DOMAIN      307    320       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    321    342       4 (POTENTIAL).
FT   DOMAIN      343    361       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    362    382       5 (POTENTIAL).
FT   DOMAIN      383    409       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    410    428       6 (POTENTIAL).
FT   DOMAIN      429    440       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    441    463       7 (POTENTIAL).
FT   DOMAIN      464    591       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    176    176       N-LINKED (GLCNAC...)  (POTENTIAL).
SQ   SEQUENCE   591 AA;  66260 MW;  21944F3051B9E9C1 CRC64;
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Query Match   11.5%;   Score 75;   DB 1; Length 591;
Best Local Similarity   32.5%;   Pred. No. 2.6;
Matches   25;   Conservative   12;   Mismatches   26;   Indels   14;   Gaps   5;

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Qy    4  DVASEFRKKWNKWALSRG-KRELRM-SSSYP------TGLADV--KAG--PAQTLIRP  49
            :| |||||:|::|  || |||||   || :   :| :||    |
Db  465  EVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVNVGPRAGLSLPLSPRLPP 524

Qy   50  QDMKGASRSPEDSSPDA  66
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Db   525  ATTNGHSQLPGHAKPGA  541
             |:.| .:| |:| :||
RESULT 9
FIBB_PETMA
ID   FIBB_PETMA     STANDARD;      PRT;    477 AA.
AC   P02678;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragments).
OS   Petromyzon marinus (Sea lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Petromyzon.
OX   NCBI_TaxID=7757;
RN   [1]
RP   SEQUENCE OF 1-36.
RX   MEDLINE=77065679; PubMed=999898;
RA   Cottrell B.A., Doolittle R.F.;
RT   "Amino acid sequences of lamprey fibrinopeptides A and B and
RT   characterization of the junctions split by lamprey and mammalian
RT   thrombins.";
RL   Biochim. Biophys. Acta 453:426-438(1976).
RN   [2]
RP   SEQUENCE OF 37-477 FROM N.A.
RX   MEDLINE=87076582; PubMed=3790537;
RA   Bohonus V.L., Doolittle R.F., Pontes M., Strong D.D.;
RT   "Complementary DNA sequence of lamprey fibrinogen beta chain.";
RL   Biochemistry 25:6512-6516(1986).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC       CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
CC       EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC       (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC       MONOMERS.
CC   -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC   --------------------------------------------------------------------
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CC   --------------------------------------------------------------------
DR   EMBL; M14773; AAA49261.1; -.
DR   PIR; A03124; A03124.
DR   PIR; A25052; A25052.
DR   HSSP; P02675; 1FZF.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Blood coagulation; Plasma; Sulfation; Glycoprotein.
FT   PEPTIDE       1     36       FIBRINOPEPTIDE B.
FT   NON_CONS     36     37
FT   CHAIN       <37    477       FIBRINOGEN BETA CHAIN.
FT   MOD_RES      13     13       SULFATION.
FT   CARBOHYD     27     27       N-LINKED (GLCNAC...).
FT   DISULFID     84     84       INTERCHAIN (WITH THE ALPHA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID     95     95       INTERCHAIN (WITH THE ALPHA CHAIN)
FT                                (BY SIMILARITY).
FT   DISULFID     99     99       INTERCHAIN (WITH THE GAMMA CHAIN)
FT                                (BY SIMILARITY).
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FT   DISULFID     212    212       INTERCHAIN (WITH THE ALPHA CHAIN)
FT                                 (BY SIMILARITY).
FT   DISULFID     216    216       INTERCHAIN (WITH THE GAMMA CHAIN)
FT                                 (BY SIMILARITY).
FT   DISULFID     220    304       BY SIMILARITY.
FT   DISULFID     230    259       BY SIMILARITY.
FT   DISULFID     412    425       BY SIMILARITY.
SQ   SEQUENCE   477 AA;  54270 MW;  B8A95E7E32D09D18 CRC64;

Query Match      10.9%;  Score 71.5;  DB 1;  Length 477;
Best Local Similarity  26.3%;  Pred. No. 4.9;
Matches  36;  Conservative  15;  Mismatches  59;  Indels  27;  Gaps    7;

Qy      2 RLDVASEFRKKWNKW-------ALSRGKRELRMSSSYYTGLADV----KAGPAQTLIRPQ 50
          |:|:|| :|  |    |:|    ||  ||   :|   || | |  |     || :|||
Db    274 RVDGSSNFARDWNTYKAEFGNIAFGNGKSICNIPGEYWLGTKTVHQLTKQHTQQVLFDMS 333

Qy     51 DMKG------ASRSPEDSSPDAARIRVKRYRQSMNN--FQGLRSFGCRFGTCTVQKIAH 101
          |:|             ||   | |: || | |  |       |:
Db    334 DWEGSSVYAQYASFRPENEA-QGYRLWVEDYSGNAGNALLEGATQLMGDNRTWTI----H 388

Qy    102 QIYQFT--DKDKDNVAP 116
          ||:     |:||| ||
Db    389 NGMQFSTFDRDNDNWNP 405

RESULT 10
FA5_HUMAN
ID   FA5_HUMAN       STANDARD;       PRT;   2224 AA.
AC   P12259; Q14285;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Coagulation factor V precursor (Activated protein C cofactor).
GN   F5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9232668; PubMed=1567832;
RA   Cripe L.D., Moore K.D., Kane W.H.;
RT   "Structure of the gene for human coagulation factor V.";
RL   Biochemistry 31:3777-3785(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87260886; PubMed=3110773;
RA   Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
RA   Hewick R.M., Kaufman R.J., Mann K.G.;
RT   "Complete cDNA and derived amino acid sequence of human factor V.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
RN   [3]
RP   SEQUENCE OF 1-1600 FROM N.A.
RX   MEDLINE=88107560; PubMed=2827731;
RA   Kane W.H., Ichinose A., Hagen F.S., Davie E.W.;
RT   "Cloning of cDNAs coding for the heavy chain region and connecting
RT   region of human factor V, a blood coagulation factor with four types
RT   of internal repeats.";
RL   Biochemistry 26:6508-6514(1987).
RN   [4]
RP   SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A.
RX   MEDLINE=86313665; PubMed=3092220;
RA   Kane W.H., Davie E.W.;
RT   "Cloning of a cDNA coding for human factor V, a blood coagulation
RT   factor homologous to factor VIII and ceruloplasmin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
RN   [5]
RP   PARTIAL SEQUENCE FROM N.A.
RC   TISSUE=Fibroblast;
RX   MEDLINE=93203619; PubMed=8454869;
RA   Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
RA   Edgington T.S.;
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RT   "The serine protease cofactor factor V is synthesized by
RT   lymphocytes.";
RL   J. Immunol. 150:2992-3001(1993).
RN   [6]
RP   SULFATION.
RX   MEDLINE=94264012; PubMed=8204629;
RA   Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
RA   Kaufman R.J.;
RT   "Posttranslational sulfation of factor V is required for efficient
RT   thrombin cleavage and activation and for full procoagulant activity.";
RL   Biochemistry 33:6952-6959(1994).
RN   [7]
RP   SULFATION.
RX   MEDLINE=90366699; PubMed=2168225;
RA   Hortin G.L.;
RT   "Sulfation of tyrosine residues in coagulation factor V.";
RL   Blood 76:946-952(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
RX   MEDLINE=2005169; PubMed=10586886;
RA   Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
RA   Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
RA   Fuentes-Prior P.;
RT   "Crystal structures of the membrane-binding C2 domain of human
RT   coagulation factor V.";
RL   Nature 402:434-439(1999).
RN   [9]
RP   VARIANT APCR GLN-534.
RX   MEDLINE=94217810; PubMed=8164741;
RA   Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
RA   Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
RT   "Mutation in blood coagulation factor V associated with resistance to
RT   activated protein C.";
RL   Nature 369:64-67(1994).
CC   -!- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
CC       WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
CC   -!- SUBUNIT: Factor Va is composed of a heavy chain and a light
CC       chain, noncovalently bound. The interaction between the two chains
CC       is calcium-dependent.
CC   -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
CC       REPEATS.
CC   -!- PTM: Thrombin activates factor V proteolytically to the active
CC       cofactor, factor Va (formation of a heavy chain at the N-
CC       terminus and a light chain at the C-terminus).
CC   -!- PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND
CC       ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.
CC   -!- DISEASE: OWREN PARAHEMOPHILIA, AN HEMORRHAGIC DIASTESIS, IS DUE
CC       TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN F5 RESULTS IN A
CC       FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
CC       MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT
CC       A SLIGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
CC       IMPLANTATION.
CC   -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
CC       2 PLASTOCYANIN-LIKE REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC   -!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
CC
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DR   EMBL; L32779; AAB59401.1;  -.
DR   EMBL; L32755; AAB59401.1;  JOINED.
DR   EMBL; L32756; AAB59401.1;  JOINED.
DR   EMBL; L32757; AAB59401.1;  JOINED.
DR   EMBL; L32758; AAB59401.1;  JOINED.
DR   EMBL; L32759; AAB59401.1;  JOINED.
DR   EMBL; L32760; AAB59401.1;  JOINED.
DR   EMBL; L32761; AAB59401.1;  JOINED.
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DR   EMBL; L32762; AAB59401.1; JOINED.
DR   EMBL; L32763; AAB59401.1; JOINED.
DR   EMBL; L32764; AAB59401.1; JOINED.
DR   EMBL; L32765; AAB59401.1; JOINED.
DR   EMBL; L32766; AAB59401.1; JOINED.
DR   EMBL; L32767; AAB59401.1; JOINED.
DR   EMBL; L32768; AAB59401.1; JOINED.
DR   EMBL; L32769; AAB59401.1; JOINED.
DR   EMBL; L32770; AAB59401.1; JOINED.
DR   EMBL; L32771; AAB59401.1; JOINED.
DR   EMBL; L32772; AAB59401.1; JOINED.
DR   EMBL; L32773; AAB59401.1; JOINED.
DR   EMBL; L32774; AAB59401.1; JOINED.
DR   EMBL; L32775; AAB59401.1; JOINED.
DR   EMBL; L32776; AAB59401.1; JOINED.
DR   EMBL; L32777; AAB59401.1; JOINED.
DR   EMBL; M16967; AAA24424.1; -.
DR   EMBL; M14335; AAB59532.1; -.
DR   PIR; A25897; A25897.
DR   PIR; A28028; A28028.
DR   PDB; 1CZS; 26-NOV-99.
DR   PDB; 1CZT; 26-NOV-99.
DR   PDB; 1CZV; 26-NOV-99.
DR   MIM; 134400; -.
DR   MIM; 188055; -.
DR   MIM; 227310; -.
DR   MIM; 227400; -.
DR   InterPro; IPR001117; Cu-oxidase.
DR   InterPro; IPR000421; FA58_C.
DR   Pfam; PF00394; Cu-oxidase; 3.
DR   Pfam; PF00754; F5_F8_type_C; 2.
DR   SMART; SM00231; FA58C; 2.
DR   PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR   PROSITE; PS01285; FA58C_1; 2.
DR   PROSITE; PS01286; FA58C_2; 2.
KW   Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
KW   Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
FT   SIGNAL        1     28
FT   CHAIN        29   2224       COAGULATION FACTOR V.
FT   CHAIN        29    737       HEAVY CHAIN.
FT   PEPTIDE     738   1573       ACTIVATION PEPTIDE (CONNECTING REGION).
FT   CHAIN      1574   2224       LIGHT CHAIN.
FT   DOMAIN       30    329       F5/8 TYPE A 1.
FT   DOMAIN       30    193       PLASTOCYANIN-LIKE 1.
FT   DOMAIN      203    329       PLASTOCYANIN-LIKE 2.
FT   DOMAIN      348    684       F5/8 TYPE A 2.
FT   DOMAIN      348    526       PLASTOCYANIN-LIKE 3.
FT   DOMAIN      536    684       PLASTOCYANIN-LIKE 4.
FT   DOMAIN      692   1573       B.
FT   DOMAIN      895    928       2 X 17 AA TANDEM REPEATS.
FT   REPEAT      895    911       1-1.
FT   REPEAT      912    928       1-2.
FT   SIMILAR    1135   1148       TO 14 AA REPEATS IN BOVINE FA5.
FT   DOMAIN     1185   1501       35 X 9 AA APPROXIMATE TANDEM REPEATS OF
FT                                [TNP]-L-S-P-D-L-S-Q-T.
FT   REPEAT     1185   1193       2-1.
FT   REPEAT     1194   1202       2-2.
FT   REPEAT     1203   1211       2-3.
FT   REPEAT     1212   1220       2-4.
FT   REPEAT     1221   1229       2-5.
FT   REPEAT     1230   1238       2-6.
FT   REPEAT     1239   1247       2-7.
FT   REPEAT     1248   1256       2-8.
FT   REPEAT     1257   1265       2-9.
FT   REPEAT     1266   1274       2-10.
FT   REPEAT     1275   1283       2-11.
FT   REPEAT     1284   1292       2-12.
FT   REPEAT     1293   1301       2-13.
FT   REPEAT     1302   1310       2-14.
FT   REPEAT     1311   1319       2-15.
FT   REPEAT     1320   1328       2-16.
FT   REPEAT     1329   1337       2-17.
FT   REPEAT     1338   1346       2-18.
FT   REPEAT     1347   1355       2-19.
FT   REPEAT     1356   1364       2-20.
FT   REPEAT     1365   1373       2-21.
FT   REPEAT     1374   1382       2-22.
FT   REPEAT     1383   1391       2-23.
FT   REPEAT     1392   1400       2-24.
FT   REPEAT     1401   1409       2-25.
FT   REPEAT     1410   1418       2-26.

Query Match             10.8%;  Score 71;  DB 1;  Length 2224;
Best Local Similarity   22.6%;  Pred. No. 30;
Matches   28;  Conservative  20;  Mismatches  52;  Indels  24;  Gaps   3;

Qy     4  DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED--  61
          |  |::|  | |::.:: :  ::   :|   :.:|:  |::|:  | |:|::  |::||
Db   873  DQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRPWEDLPSQDTGSPSRMRPWKDPPSDLL  932

Qy    62  --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK  119
            ::|:|:|:         :: :|::|||:.   |:.|::|::||
Db   933  LLKQSNSSKILVGRWHLAS---------------EKGSYEIIQ--DTDEDTAVNNWL  972

Qy   120  ISPQ 123
          |||
Db   973  ISPQ 976

RESULT 11
PRI1_SCHPO
ID   PRI1_SCHPO   STANDARD;   PRT;   454 AA.
AC   O14215;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Probable DNA primase small subunit (EC 2.7.7.-).
GN   SPAC6B12.10C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
CC       RNA PRIMERS FOR THE OKAZAKI FRAGMENTS MADE DURING DISCONTINUOUS
CC       DNA REPLICATION.
CC   -!- SUBUNIT: HETERODIMER OF A SMALL SUBUNIT AND A LARGE SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE EUKARYOTIC PRIMASE SMALL SUBUNIT
CC       FAMILY.
```

```
DR   EMBL; Z98531; CAB11078.1; -.
DR   InterPro; IPR002755; DNA_primase_S.
DR   Pfam; PF01896; DNA_primase_S; 1.
KW   Transferase; DNA replication; DNA-directed RNA polymerase; Primosome.
FT   ACT_SITE     66     66       POTENTIAL.
FT   ACT_SITE    131    131       POTENTIAL.
FT   ACT_SITE    133    133       POTENTIAL.
FT   METAL       143    143       POTENTIAL.
FT   METAL       144    144       POTENTIAL.
FT   METAL       150    150       POTENTIAL.
FT   METAL       153    153       POTENTIAL.
SQ   SEQUENCE   454 AA;  52009 MW;  71526FFAF7C2BBFA CRC64;
```

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Query Match         10.5%;  Score 69;  DB 1;  Length 454;
Best Local Similarity  24.4%;  Pred. No. 8.4;
Matches  32;  Conservative  20;  Mismatches  43;  Indels  36;  Gaps  6;

Qy    4  DVASEFRKKW--------NKWA----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP   49
            |:||  |||||         |||:  ||   |:|     ||:|||   |||:|
Db  275  DLASALRKKWEVDPERSSKNKWSDIDTVLASGS---TASISPSVIAIAKQDIVLTYLYP  330

Qy   50  ------QDMKGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ  102
                   :||  :|   ||   |:|: |||  :   ||
Db  331  RLDVEVSRHLNHLLKSPFCVHPGTSRVCVPIDIERMDSFNPLK------VPTVNDLLQE  383

Qy  103  IYQFTDKDKDN  113
             :   ||   |
Db  384  L---DKNSQN  390
```

RESULT 12
FIBB_RAT
ID   FIBB_RAT   STANDARD;   PRT;   479 AA.
AC   P14480;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN   FGB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX   MEDLINE=95143386; PubMed=7841303;
RA   Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
RT   "Cloning of the complete coding sequence of rat fibrinogen B beta
RT   chain cDNA: interspecies conservation of fibrin beta 15-42 primary
RT   structure.";
RL   Blood Coagul. Fibrinolysis 5:487-496(1994).
RN   [2]
RP   SEQUENCE OF 1-26 FROM N.A.
RX   MEDLINE=84194000; PubMed=6232608;
RA   Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT   "Potential basis for regulation of the coordinately expressed
RT   fibrinogen genes: homology in the 5' flanking regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
RN   [3]
RP   SEQUENCE OF 19-32.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [4]
RP   SEQUENCE OF 183-479 FROM N.A.
RX   MEDLINE=89378771; PubMed=2673932;
RA   Eastman E.M., Gilula N.B.;
RT   "Cloning and characterization of a cDNA for the B beta chain of rat
RT   fibrinogen: evolutionary conservation of translated and
RT   3' untranslated sequences.";
RL   Gene 79:151-158(1989).
RN   [5]
RP   SEQUENCE OF 425-479 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=87134033; PubMed=3817019;
RA   Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
RT   "Molecular cloning of mRNA sequences transiently induced during rat
RT   liver regeneration.";
RL   Exp. Cell Res. 169:47-56(1987).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC   POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC   AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC   (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC   THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC   CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC   RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC   -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

DR   EMBL; U05675; AAA64866.1; -.
DR   EMBL; M27220; AAA41160.1; -.
DR   EMBL; K01336; AAA98625.1; -.
DR   EMBL; M35602; AAA41159.1; -.
DR   PIR; A05299; A05299.
DR   PIR; PE0010; PE0010.
DR   HSSP; P02675; 1FZE.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   Pfam; PF00147; fibrinogen_C; 1.
DR   SMART; SM00186; FBG; 1.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW   Blood coagulation; Plasma; Glycoprotein; Signal.
FT   SIGNAL   1   18
FT   CHAIN   19   479   FIBRINOGEN BETA CHAIN.
FT   PEPTIDE   19   32   FIBRINOPEPTIDE B.
FT   DISULFID   211   211   INTERCHAIN (WITH THE ALPHA CHAIN)
FT   (BY SIMILARITY).
FT   DISULFID   215   215   INTERCHAIN (WITH THE GAMMA CHAIN)
FT   (BY SIMILARITY).
FT   DISULFID   219   304   BY SIMILARITY.
FT   DISULFID   229   258   BY SIMILARITY.
FT   DISULFID   412   425   BY SIMILARITY.
FT   CARBOHYD   382   382   N-LINKED (GLCNAC...). (POTENTIAL).
FT   CONFLICT   28   30   LSI -> ILS (IN REF. 3).
FT   CONFLICT   439   439   L -> Q (IN REF. 5).
FT   CONFLICT   441   441   S -> T (IN REF. 5).
FT   CONFLICT   445   445   S -> A (IN REF. 5).
FT   CONFLICT   467   467   R -> T (IN REF. 5).
FT   CONFLICT   475   475   V -> F (IN REF. 5).
SQ   SEQUENCE   479 AA; 54303 MW; EC8C6DB77C3E0EC0 CRC64;

```
Query Match         10.5%;  Score 68.5;  DB 1;  Length 479;
Best Local Similarity  20.9%;  Pred. No. 10;
Matches  31;  Conservative  23;  Mismatches  63;  Indels  31;  Gaps  6;

Qy    2  RLDVASEFRKRKWNKWALSRG--------KRELRMSSSYPTGLADV---KAGPAQTLIRP   49
            |   |:|   |  :       |        |:|   |||||   |||||     | |:|
Db  273  RQDGSVDFGRKWDPYKKGFGNIATNEDTKKYCGLPCEYWLGNDKISQLTRIGPTELLIEM  332

Qy   50  QDMKGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG------TCTVQKLA  100
            :|||         |:|   ||   ||||         |:|:|     ||:|
Db  333  EDWKG-DKVKAHYGGFTVQTEANKYQVSVNKYKGTAGNALMEGASQLVGENRTMTI----  387

Qy  101  HQIYQFTDKDKDN-----VAPRSKISPQ  123
            ||         |:   |:|     |  |:|
Db  388  HNGMFFSTYDRDNDGWVTTDPRKQCSKE  415
```

RESULT 13
VP13_YEAST
ID   VP13_YEAST   STANDARD;   PRT;   3144 AA.
AC   Q07778; O00040;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Vacuolar protein sorting-associated protein VPS13.
GN   VPS13 OR SOI1 OR YLL040C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

```
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RA   Brickner J.H., Fuller R.S.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-1360 FROM N.A.
RA   Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H.,
RA   Moestl D.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1095-3144 FROM N.A.
RA   Wedler H., Wedler E., Scharfe M., Wambutt R.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   CHARACTERIZATION.
RA   Luo W., Chang A.;
RL   Unpublished observations (XXX-1997).
CC   -!- FUNCTION: PROMOTES ENDOSOMAL CYCLING OF TGN MEMBRANE PROTEINS BY
CC       MODULATING THE FUNCTION OF TWO CYTOSOLIC TGN LOCALIZATION SIGNALS.
CC   -!- SIMILARITY: SOME, TO S.POMBE SPBC16C5.02C.
CC   --------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; AF001317; AAC08284.1; -.
DR   EMBL; Z73144; CAA97490.1; -.
DR   EMBL; Z73145; CAA97491.1; -.
DR   SGD; S0003963; VPS13.
SQ   SEQUENCE   3144 AA;   357843 MW;   BEE9B55BA2AD515B CRC64;

Query Match             10.5%;   Score 68.5;   DB 1;   Length 3144;
Best Local Similarity   28.0%;   Pred. No. 82;
Matches   37;   Conservative   20;   Mismatches   36;   Indels   39;   Gaps   10;

Qy    19  SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE---DSSPDAARIR   70
Db  1354  SGGKGEIKSPSPDPASL---SSESERTATPQSLQGSNKSNIKNPEQKYLDFSFKAPKIA 1409

Qy    71  VKRYRQ-----SMNN------FQGLRSFGCRFG---TCTVQKLAHQIYQFTDKD-----K 111
Db  1410  LTLYNKTKGVTSLNDCGLTRIMFQDI---GCSLGLKNDGTVDGQAH-VAAFRIEDVRNIK 1465

Qy   112  DN----VAPRSK 119
Db  1466  DNKHTELIPKSK 1477

RESULT 14
MOXJ_METEX
ID   MOXJ_METEX     STANDARD;     PRT;     300 AA.
AC   P16028;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MoxJ protein precursor.
GN   MOXJ.
OS   Methylobacterium extorquens.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Methylobacterium group; Methylobacterium.
OX   NCBI_TaxID=408;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AM1 / NCIB 9133;
RX   MEDLINE=90337342; PubMed=2116368;
RA   Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidstrom M.E.;
```

```
RT   "Nucleotide sequence of the Methylobacterium extorquens AM1 moxF and
RT   moxJ genes involved in methanol oxidation.";
RL   Gene 90:173-176(1990).
CC   -!- FUNCTION: MAY BE INVOLVED IN THE ASSEMBLAGE OF ACTIVE METHANOL
CC       DEHYDROGENASE AND/OR ITS COFACTOR PQQ IN THE PERIPLASM.
CC   -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC   -!- SIMILARITY: WITH THE CORRESPONDING PROTEIN IN P.DENITRIFICANS.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; M31108; AAA25381.1; -.
DR   PIR; JQ0707; JQ0707.
DR   InterPro; IPR001638; SBP_bac_3.
DR   SMART; SM00062; PBPb; 1.
KW   Signal; Methanol utilization; Periplasmic.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    300       MOXJ PROTEIN.
SQ   SEQUENCE   300 AA;   32425 MW;   BC347551D51B542F CRC64;

Query Match             10.3%;   Score 67.5;   DB 1;   Length 300;
Best Local Similarity   30.1%;   Pred. No. 7.6;
Matches   28;   Conservative   14;   Mismatches   36;   Indels   15;   Gaps   5;

Qy    17  ALSRGKRELRMS-----SSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVK  72
Db     2  SLVNGRRRTAASVVALTAALTALALCA-PAQA----QDTKATSKAEAAKPDAGTLRVC    56

Qy    73  RYRQ---SMNNFQGLRSFGCRFGTCTVQKLAHQ 102
Db    57  AAEQPPLSMKDGSGLEN---RIATTVAEAMGRK  86

RESULT 15
SLS6_BRAOL
ID   SLS6_BRAOL     STANDARD;     PRT;     436 AA.
AC   P07761;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   S-locus-specific glycoprotein S6 precursor (SLSG-6).
GN   SLSG.
OS   Brassica oleracea (Cauliflower).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3712;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
RT   "Amino-acid sequence of glycoproteins encoded by three alleles of the
RT   S locus of Brassica oleracea.";
RL   Nature 326:617-619(1987).
RN   [2]
RP   SEQUENCE OF 22-435 FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RT   "A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
RT   oleracea.";
RL   Nature 318:263-267(1985).
RN   [3]
RP   ERRATUM.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RL   Nature 326:523-523(1987).
CC   -!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC       (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
CC   -!- TISSUE SPECIFICITY: STIGMA.
CC   -!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
CC       B.OLERACEA.
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CC   -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
CC       KINASE RECEPTOR (ZMPK1).
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; Y00268; CAA68375.1; -.
DR   EMBL; X03170; CAA26934.1; ALT_INIT.
DR   PIR; A27827; A27827.
DR   InterPro; IPR001480; B_lectin.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR000858; Slocus_glycop.
DR   Pfam; PF01453; Agglutinin; 1.
DR   Pfam; PF00954; S_locus_glycop; 1.
DR   SMART; SM00108; B_lectin; 1.
DR   SMART; SM00473; PAN_AP; 1.
KW   Self-incompatibility; Glycoprotein; Polymorphism; Signal.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN        32    436       S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
FT   CARBOHYD     46     46       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     64     64       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    121    121       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    245    245       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    261    261       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    390    390       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   436 AA;  49779 MW;  E2332635B885A515 CRC64;

Query Match             10.2%;  Score 67;  DB 1;  Length 436;
Best Local Similarity   25.3%;  Pred. No. 13;
Matches   42;  Conservative   22;  Mismatches   42;  Indels   60;  Gaps   11;

Qy      2 RLDVASEFRKKWNKWALSRGKRELRMSSS------------YPTG--LADVKAGPAQTLI 47
            || |:|              || |  || :|      |||     | |:: |
Db    128 RLPVAEL--------LSNGNFVMRDSSNNDASEYLWQSFDYPTDTLLPEMKLG------ 173

Qy     48 RPQDMK-------GASRSPEDSSPDAARIRVKRYRQSMNNF---QGL-----RS--FGCR 90
           |:|         || |:| |   :| |  | :     |     || |:     || ||
Db    174 --YDLKTGLNRFLTSWRSSDD--PSSGDFSYKLETRSLPEFYLWHGIFPMHRSGPWNGVR 229

Qy     91 F-GTCTVQKLAHQIYQFTDKDKD---------NVAPRSKISPQGY 125
           | |              ||: :|          :: :| :|| :||
Db    230 FSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
```

Search completed: October 17, 2002, 15:21:36
Job time : 7.51466 secs

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OM protein - protein search, using sw model

```
                Copyright  GenCore version 5.1.3
                Copyright (c) 1993 - 2002  Compugen Ltd.

Run on:         October 17, 2002, 15:20:13 ; Search time 11.8078 Seconds
                                            (without alignments)
                                            1017.222 Million cell updates/sec

Title:          US-10-018-924-2_COPY_22_146
Perfect score:  655
Sequence:       1 ARLDVASEFRKKWNKWALSR.........FTDKDKDNVAPRSKISPQGY 125

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:    283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_71:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	655	100.0	185	2	JN0684	adrenomedullin pre
2	611	93.3	188	2	S41600	adrenomedullin - p
3	458.5	70.0	185	2	JN0766	adrenomedullin pre
4	77	11.8	591	2	S44203	parathyroid hormon
5	76	11.6	589	2	I59297	parathyroid hormon
6	75	11.5	591	2	I54195	parathyroid hormon
7	75	11.5	1051	2	C95367	conserved hypothet
8	71.5	10.9	479	2	A25052	fibrinogen beta ch
9	71	10.8	2224	1	KFHU5	coagulation factor
10	69	10.5	380	2	T08036	GTP-binding regula
11	69	10.5	454	2	T39017	probable DNA prima
12	68.5	10.5	328	2	A05299	fibrinogen beta ch
13	68.5	10.5	926	2	F88632	protein F56B3.4 [I
14	68.5	10.5	1196	2	H86389	hypothetical prote
15	68.5	10.5	3144	2	S64791	VPS13 protein - ye
16	68	10.4	168	2	T28776	hypothetical prote
17	68	10.4	347	2	T31120	rod shape-determin
18	68	10.4	858	2	T09344	probable phospholi
19	67.5	10.3	300	2	JQ0707	methanol oxidation
20	67	10.2	436	2	A27827	S-locus-specific g
21	66.5	10.2	1766	2	S03701	141K protein - pea
22	66.5	10.1	380	2	T02085	GTP-binding protei
23	66	10.1	397	2	S30023	antiviral protein
24	66	10.1	731	2	JC7701	ARHGAP9 protein -
25	66	10.1	1050	2	S57488	fimbrial protein p
26	65.5	10.0	297	2	T47857	myb protein-like -
27	65.5	10.0	451	2	S13337	tubulin alpha-2 ch
28	65.5	10.0	497	2	S43745	phosphatidylinosit
29	65.5	10.0	532	2	JC1392	monophenol monooxy
30	65.5	10.0	727	2	AD1868	hypothetical prote
31	65.5	10.0	1116	2	T16112	hypothetical prote
32	65	9.9	253	2	H81690	conserved hypothet
33	65	9.9	305	2	T24283	hypothetical prote
34	65	9.9	380	2	S71574	tubulin alpha chai
35	65	9.9	428	2	G75453	hypothetical prote
36	65	9.9	485	2	JQ1957	glucagon receptor
37	65	9.9	867	2	G81856	membrane alanyl am
38	65	9.9	924	2	T06636	hypothetical prote
39	65	9.9	1017	2	PC4035	cell-cycle-depende
40	65	9.9	1252	2	H71529	DNA-directed RNA p
41	65	9.9	1252	2	G81686	DNA-directed RNA p
42	64.5	9.8	381	2	D70669	coenzyme F420-depe
43	64.5	9.8	409	2	B25156	cellulase (EC 3.2.
44	64.5	9.8	417	2	T51467	glucose 6 phosphat
45	64.5	9.8	444	2	T25413	hypothetical prote

ALIGNMENTS

```
RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351, MUID:94354869
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A;Reference number: JN0684; MUID:93343928
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A;Accession: JN0476; MUID:93249425
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;147-185/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match       100.0%;   Score 655;   DB 2;   Length 185;
Best Local Similarity    100.0%;   Pred. No. 2.6e-61;
Matches  125;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
```

RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA enco
A;Reference number: S41600; MUID:94139945
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

Query Match   93.3%; Score 611; DB 2; Length 188;
Best Local Similarity   91.2%; Pred. No. 1.1e-56;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy   1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
           ||||||:||||||||||||||||||||||||||||:|:||||||:|||||||:||||||:
Db   22 ARLDVAAEFRKKWNKWALSRGKRELRMSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141

Qy   121 SPQGY 125
           |||||
Db   142 SPQGY 146

RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

Query Match   70.0%; Score 458.5; DB 2; Length 185;
Best Local Similarity   72.8%; Pred. No. 1.1e-40;
Matches 91; Conservative 10; Mismatches 21; Indels 3; Gaps 2;

Qy   1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
           |||| :::|||||||||||||||||: ::: :|| :: : : || : :: :||
Db   22 ARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
           |: |:||||||||||||||: : ||||:||||||||:||||||||||||||||: :||:
Db   81 ASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDQGMAPRNKI 138

Qy   121 SPQGY 125
           |||||
Db   139 SPQGY 143

RESULT 4
S44203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C;Accession: S44203
R;Karpelen, M.; van Dijk, T.B.; Hoeljmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boon
submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related
A;Reference number: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <KAR>
A;Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
C;Superfamily: glucagon receptor

Query Match   11.8%; Score 77; DB 2; Length 591;
Best Local Similarity   32.5%; Pred. No. 4.3;
Matches 26; Conservative 12; Mismatches 28; Indels 14; Gaps 5;

Qy   4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP------TGLADV-KAG---PAQTLIRP 49
           :|::||:|::| || ::|: || :|| :: | :|| : ||:: :|
Db   465 EVQAEIRKSWSRWTLALDFKRKARSGSSYSYGPMGAHTSVTNVGPRAGLSLPLSPRLLP 524

Qy   50 QDMKGASRSPEDSSPDAARI 69
           :|: :||: ||: |
Db   525 ATTNGHSQLPGHAKPGAPAI 544

RESULT 5
I59297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I59297
R;McCuaig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A;Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathy
A;Reference number: I59297; MUID:94255468
A;Accession: I59297
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-589 <RES>
A;Cross-references: GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151
C;Genetics:
A;Gene: PTHR
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C;Superfamily: glucagon receptor

Query Match   11.6%; Score 76; DB 2; Length 589;
Best Local Similarity   32.5%; Pred. No. 5.4;
Matches 26; Conservative 12; Mismatches 28; Indels 14; Gaps 5;

Qy   4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP------TGLADV-KAG--PAQTLIRP 49
           :|::||:|::| || ::|: :: :|| ::| | :|

Db 463 NVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLLP 522

Qy   50 QDMKGASRSPEDSSPDAARI 69

Db 523 ATTNGHSQLPGHAKPGAPAI 542

RESULT 6
I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C;Accession: I54195; A42698
R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (
and rat genomes.
A;Reference number: I54195; MUID:94292182
A;Accession: I54195
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-591 <RES>
A;Cross-references: GB:L19475; NID:g467316; PIDN:AAA68098.1; PID:g467317
R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
A;Reference number: A42698; MUID:92212903
A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-585,'G,'587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:92187)
C;Superfamily: glucagon receptor

Query Match   11.5%; Score 75; DB 2; Length 591;
Best Local Similarity   32.5%; Pred. No. 6.9;
Matches   25; Conservative 12; Mismatches 26; Indels 14; Gaps 5;

Qy   4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP------TGLADV--KAG---PAQTLIRP 49
           | |:|||:|| |: | | |: | :| :|| |:|| |:|
Db 465 EVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP 524

Qy   50 QDMKGASRSPEDSSPDA 66
           ||:|| ::| |
Db 525 ATTNGHSQLPGHAKPGA 541

RESULT 7
C95367
conserved hypothetical protein SMa1548 [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: C95367
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1051 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65501.1; PID:g14523974; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMa1548
A;Genome: plasmid

Query Match   11.5%; Score 75; DB 2; Length 1051;
Best Local Similarity   26.9%; Pred. No. 13;
Matches   32; Conservative 14; Mismatches 63; Indels 10; Gaps 4;

Qy   5 VASEFRKK-----WNKWALSRGKRELRMSSS---YPTGLADVKAGPAQTLIRPQDMKGAS 56
           |||:||| :|:| |: |: :|: : |||||||:||:|||||
Db 320 VRSEYRLRRADGSW-AWVIDVGQPRFSADGTFLGYVGSVLDITERRAAE-IAQQEAQAFI 377

Qy   57 RSPEDSSPDAARIRVKRYRQSMNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVA 115
           :| ::| :| ||::| :| ||::: |||| | | :|:| |
Db 378 RSIFDSSPDCVRVLDMEGRPLLMNEAGRRIFGLNEGAPVTGQTWDSIGRASDADKVEAA 436

RESULT 8
A25052
fibrinogen beta chain - sea lamprey (fragments)
N;Contains: fibrinopeptide B
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C;Accession: A25052; A03124; B03124
R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A;Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A;Reference number: A25052; MUID:8076582
A;Accession: A25052
A;Molecule type: mRNA
A;Residues: 39-479 <BOH>
A;Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
R;Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A;Reference number: A03120; MUID:77065679
A;Accession: A03124
A;Molecule type: protein
A;Residues: 1-36 <COT1>
A;Accession: B03124
A;Molecule type: protein
A;Residues: 37-42 <COT2>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C;Keywords: blood coagulation; glycoprotein; sulfoprotein
F;1-36/Product: fibrinopeptide B #status experimental <FPB>
F;37-479/Product: fibrin beta chain #status experimental <FDR>
F;90-219/Domain: fibrinogen disulfide ring homology <FDR>
F;229-477/Domain: fibrinogen beta/gamma homology <FBG>
F;13/Binding site: sulfate (Tyr) (covalent) #status experimental
F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   10.9%; Score 71.5; DB 2; Length 479;
Best Local Similarity   26.3%; Pred. No. 13;
Matches   36; Conservative 15; Mismatches 59; Indels 27; Gaps 7;

Qy   2 RLDVASEFRKKWNKW------ALSRGKRELRMSSSYPTGLADV---KAGPAQTLIRPQ 50
           |:| :||:|| :| |:| :|||:|||| |||||||:||
Db 276 RVDGSSNFARDWNTYKAEFGNIAFGNGKSICNIPGEYWLGTKTVHQLFKQHTQQVLFDMS 335

Qy   51 DMKG------ASRSPEDSSPDAARIRVKRYRQSMNN--FQGLRSFGCRFGTCTVQKLAH 101
           |:|| :| :| ||||| | || |:: ||| | | | :| |
Db 336 DWEGSSVYAQYASFRPENEA-QGVRLWVEDYSGNAGNALLEGATQLMGDNRTMTI----H 390

Qy 102 QIYQFT--DKDKDNVAP 116
           |:|:| |:|||| |
Db 391 NGMQFSTFDRDNDNWNP 407

RESULT 9
KFHU5
coagulation factor v precursor [validated] - human

N;Alternate names: coagulation labile factor; proaccelerin
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000
C;Accession: A56172; A42344; A28028; A27498; A25897
R;Cripe, L.D.; Moore, K.D.; Kane, W.H.
Biochemistry 31, 3777-3785, 1992
A;Title: Structure of the gene for human coagulation factor V.
A;Reference number: A42344; MUID:9223 2668
A;Accession: A56172
A;Molecule type: DNA
A;Residues: 1-2224 <CRI>
A;Cross-references: GB:J05368
A;Accession: A42344
A;Molecule type: DNA
A;Residues: 48-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
2070;2111-2120;2172-2181 <CR2>
R;Jenny, R.J.; Pittman, D.D.; Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kaufm
Proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987
A;Title: Complete cDNA and derived amino acid sequence of human factor V.
A;Reference number: A28028; MUID:87260886
A;Accession: A28028
A;Molecule type: mRNA
A;Residues: 1-857,'R',859-864,'R',866-924,'E',926-1763,'I',1765-2212,'T',2214-2224 <JEN>
A;Cross-references: GB:M16967
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Biochemistry 26, 6508-6514, 1987
A;Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hum
A;Reference number: A27498; MUID:88107560
A;Accession: A27498
A;Molecule type: mRNA
A;Residues: 1-1284,'I',1286-1600 <KAN>
A;Cross-references: GB:M17785
A;Note: parts of this sequence were determined by protein sequencing
R;Kane, W.H.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 6800-6804, 1986
A;Title: Cloning of a cDNA coding for human factor V, a blood coagulation factor homolog
A;Reference number: A25897; MUID:86313665
A;Accession: A25897
A;Molecule type: mRNA
A;Residues: 1188-1215,1315-2224 <KA2>
A;Cross-references: GB:M14335
A;Note: parts of this sequence were determined by protein sequencing
R;Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
Biochemistry 34, 4118-4124, 1995
A;Title: Thrombin-catalyzed activation of recombinant human factor V.
A;Reference number: A56139; MUID:9521 0278
C;Contents: annotation; thrombin cleavage sites
C;Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
C;Genetics:
A;Gene: GDB:F5
A;Cross-references: GDB:119896; OMIM:227400
A;Map position: 1q23-1q23
A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; 65
C;Function:
A;Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa prot
A;Pathway: blood coagulation
C;Superfamily: coagulation factor v; discoidin I amino-terminal homology; ferroxidase re
C;Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasma;
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-2224/Product: coagulation factor V #status predicted <MAT>
F;29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
F;29-345/Domain: A1 <DA1>
F;33-329/Domain: ferroxidase repeat homology <FO1>
F;346-691/Domain: A2 <DA2>
F;351-684/Domain: ferroxidase repeat homology <FO2>
F;692-1573/Region: B <DOB>
F;1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F;1574-2224/Product: coagulation factor Va light chain #status experimental <VAL>
F;1574-1905/Domain: A3 <DA3>
F;1581-1905/Domain: ferroxidase repeat homology <FO3>
F;1667-1765/Region: phospholipid binding #status predicted
F;1906-2064/Domain: C1 <DC1>

F;1906-2061/Domain: discoidin I amino-terminal homology <DN1>
F;2065-2224/Domain: C2 <DC2>
F;2065-2221/Domain: discoidin I amino-terminal homology <DN2>
F;51,55,239,297,460,468,554,741,752,760,776,782,821,938,977,1074,1083,1103,1106,1479,
2070;2111-2120;2172-2181/Disulfide bonds: #sta
F;167-193,248-329,500-526,603-684,1725-1751,1907-2061,2066-2221/Disulfide bonds: #sta
F;334-335/Cleavage site: Arg-Asn (protein C) (covalent) #status predicted
F;363,693,1546/Binding site: sulfate (Tyr) (covalent) #status predicted
F;376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
F;382,1338/Binding site: carbohydrate (Asn) (covalent) #status absent
F;534-535/Cleavage site: Arg-Gly (protein C) #status predicted
F;737-738/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment
F;1046-1047/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experime
F;1573-1574/Cleavage site: Arg-Ser (thrombin) #status experimental

Query Match   10.8%; Score 71; DB 1; Length 2224;
Best Local Similarity 22.6%; Pred. No. 77;
Matches 28; Conservative 52; Mismatches 20; Indels 24; Gaps 3;

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Qy    4 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED-- 61
          |:||:|||  | ::|::| |:||  |  ::|:| |    ::|:       |:| |  |||
Db  873 DQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRPWEDLPSQDTGSPSRMRPWKDPPSDLL 932

Qy   62 --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK 119
           ||:|||||||||||||||||| |:::| |:  :|   |:  |  | :| |
Db  933 LLKQSNSSKILVGRWHLAS----------------EKGSYEIIQ--DTDEDTAVNNWL 972

Qy  120 ISPQ 123
         |||
Db  973 ISPQ 976
```

RESULT 10
T08036
GTP-binding regulatory protein beta chain - wild oat
C;Species: Avena fatua (wild oat)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-May-1999
R;Jones, H.D.; Smith, S.J.; Desikan, R.; Plakidou-Dymock, S.; Lovegrove, A.; Hooley,
Plant Cell 10, 245-254, 1998
A;Title: Heterotrimeric G proteins are implicated in gibberellin induction of a-amyla
A;Reference number: Z16226
A;Accession: T08036
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-380 <JON>
A;Cross-references: EMBL:AF033357; NID:g2935697; PIDN:AAC39373.1; PID:g2935698
C;Genetics:
A;Gene: Gb1
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F;245-278/Domain: WD repeat homology <WDR>

Query Match   10.5%; Score 69; DB 2; Length 380;
Best Local Similarity 23.6%; Pred. No. 18;
Matches 30; Conservative 18; Mismatches 41; Indels 38; Gaps 7;

```
Qy   16 WALSRGKRELRMSSSYPTG-LADV------------------KAGPAQTLIRPQDMKGASRSPED 61
          |:||:|||  | ::|::||   |:||      : ||||  :||  :|||
Db  185 WDVTTGQRISIFGGEFPSGHTADVLSLSINSLNTNMFVSGSCDTTVRLWDLRIASRA--- 241

Qy   62 SSPDAARIRVKRYRQSMNNFQGLRSF-GCRF-----GTCTV--QKLAH--QIYQFTDK 109
         |:| :|  :||  |:|:: |:: |  || :|:   :| :|
Db  242 ------VRTYHGHEGDINSVKFFPDGHRFGTGSDDGTCRLFDMRIRHQLQVYSREPD 292

Qy  110 DKDNVAP 116
         ||:|
Db  293 RNDNELP 299
```

RESULT 11
T39017
probable DNA primase small subunit - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C;Accession: T39017
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21815
A;Accession: T39017
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:Z98531; PIDN:CAB11078.1; GSPDB:GN00066; SPDB:SPAC6B12.10c
A;Experimental source: strain 972h-; cosmid c6B12
C;Genetics:
A;Gene: SPDB:SPAC6B12.10c
A;Map position: 1
A;Introns: 25/2
C;Superfamily: DNA primase 50K chain

Query Match   10.5%;   Score 69;   DB 2;   Length 454;
Best Local Similarity   24.4%;   Pred. No. 22;
Matches   32; Conservative   20; Mismatches   43; Indels   36; Gaps   6;

```
Qy     4  DVASEFRKKW--------NKWA-----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP 49
             |:||  ||||       |:  |:  :||:|:||  :: ||||||||  ||
Db   275  DLASALRKKWEVDPERSSKNKWSDIDTVLASGS----IASISPSVIAIAKQDIVLTYLYP 330

Qy    50  ------QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                :: ||  |:|  ||  ::  ||  ||  ||:|:||  |:  ||
Db   331  RLDVEVSRHLNHLLKSPFCVHPGTSRVCVPIDIERMDSFNPLK------VPTVNDLLQE 383

Qy   103  IYQFTDKDKDN 113
             ||:|
Db   384  L----DKNSQN 390
```

RESULT 12
A05299
fibrinogen beta chain precursor - rat (fragments)
N;Contains: fibrinopeptide B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 13-Aug-1999
A;Reference number: A93989; MUID:84194000
A;Accession: A05299; PE0010
R;Fowlkes, D.M.; Mullis, N.T.; Comeau, C.M.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984
A;Molecule type: DNA
A;Reference number: A05299; PE0010
R;Eastman, E.M.; Gilula, N.B.
Gene 79, 151-158, 1989
A;Title: Cloning and characterization of a cDNA for the B beta chain of rat fibrinogen:
A;Reference number: PE0010; MUID:89378771
A;Accession: PE0010
A;Molecule type: mRNA
A;Residues: 33-328 <EAS>
A;Cross-references: GB:M27220; NID:g529585; PIDN:AAA41160.1; PID:g529586
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C;Keywords: blood coagulation; glycoprotein; liver; plasma
F;33-65/Domain: fibrinogen disulfide ring homology (fragment) <FDR>
F;75-324/Domain: fibrinogen beta/gamma homology <FBG>
F;231/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   10.5%;   Score 68.5;   DB 2;   Length 328;
Best Local Similarity   20.9%;   Pred. No. 18;
Matches   31; Conservative   23; Mismatches   63; Indels   31; Gaps   6;

```
Qy     2  RLDVASEFRKKWKNWKALSRG------KRELRMSSSYPTGLADV----KAGPAQTLIRP 49
             | :|:||| :||| : :        |:|:||  :: | |:  :  || : ||
Db   122  RQDGSVDFGRKWDPYKKGFGNIATNEDTKKYCGLPGEYWLGNDKISQLTRIGPTELLIEM 181

Qy    50  QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG-------TCTVQKLA 100
             :|  :::|                  ||  ||||||||||||        |: ||
Db   182  EDWKG-DKVKAHYGGFTVQTEANKYQVSVNKYKTAGNALMEGASQLVGENRTMTI----236
```

```
Qy   101  HQIYQFTDKDKDN-----VAPRSKISPQ 123
             |  |:||    ||  :|  :
Db   237  HNGMFFSTYDRDNDGWVTDPRKQCSKE 264
```

RESULT 13
F88632
protein F56B3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
A;Accession: F88632
C;Genetics:
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: F88632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-926 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC02615.1; PID:g2854201; GSPDB:GN00022; CESP:F56
C;Genetics:
A;Gene: F56B3.4
A;Map position: 4

Query Match   10.5%;   Score 68.5;   DB 2;   Length 926;
Best Local Similarity   22.2%;   Pred. No. 54;
Matches   24; Conservative   19; Mismatches   56; Indels   9; Gaps   3;

```
Qy     2  RLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQ-DMKGASRSPE 60
             : |:|: ||:|||::|:|  :||:|:|||  : :|||:||:|   ||:|: | : |
Db   555  KLEITERFDPKLLEFLKNRGNKASEETQKKPKKISKFKASRQQK--EPENEQKGAPEPPA 612

Qy    61  DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTD 108
             |  | ||:|  :  |||  : :  ||  |  | ||| :|
Db   613  QAPP------TKVVEEMNELEVLEEYGNREDQEKYNRLATVFWKIID 654
```

RESULT 14
H86389
hypothetical protein F28B23.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
A;Accession: H86389
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H86389
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1196 <STO>
A;Cross-references: GB:AE005172; NID:g11079511; PIDN:AAG29222.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match   10.5%;   Score 68.5;   DB 2;   Length 1196;
Best Local Similarity   24.0%;   Pred. No. 72;
Matches   30; Conservative   19; Mismatches   43; Indels   33; Gaps   7;

```
Qy     3  LDVASEFRKKWNK-WALSRGKRELRMSSSYPTGLADVKAGPAQT--------------L 46
             |   :|| ||  |||:|:|| :|:||  :::||:|||: |
Db    19  VSVGALYTGSWDKKYWSSSRGKDRF----PYPVGYKAVRAHSGNTYYMEIEEGAKGPLFL 74

Qy    47  IRPQDMKGASRSPEDS-----SPDAARIRV---KRYRQSMNNFQGLRSFGCRFGTCTVQK 98
```

```
Db        75 IRYLDESWTGQTPDIAWGKLQKTDFSHLKIWHGKRFTCKMG--GMEFFG--FKNPLVQR 129
             ||   ::|:.:   |  ::::    ||::::    |::    |: ||  |   ||:
Qy        99 LAHQI 103
             |
Db       130 LLREL 134


RESULT 15
S64791
VPS13 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L0901; protein YLL040c
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
C;Accession: S64791; S64792; S14891
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64775
A;Accession: S64791
A;Molecule type: DNA
A;Residues: 1-1360 <DUE>
A;Cross-references: EMBL:Z73145; MIPS:YLL040c
A;Experimental source: strain S288C
R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64792
A;Accession: S64792
A;Molecule type: DNA
A;Residues: 1095-3144 <WED>
A;Cross-references: EMBL:Z73145; MIPS:YLL040c
A;Experimental source: strain S288C
R;Lombardo, A.; Carine, K.; Scheffler, I.E.
J. Biol. Chem. 265, 10419-10423, 1990
A;Title: Cloning and characterization of the iron-sulfur subunit gene of succinate dehyd
A;Reference number: A35435; MUID:90285165
A;Accession: S14891
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 2991-3047,'L' <LOM>
A;Cross-references: EMBL:J05487
C;Genetics:
A;Gene: SGD:VPS13; VPT2; SOI1
A;Cross-references: SGD:S0003963; MIPS:YLL040c
A;Map position: 12L
C;Function:
A;Description: involved in regulation of membrane traffic
C;Keywords: transmembrane protein
F;1084-1100/Domain: transmembrane #status predicted <TMM>

Query Match            10.5%;    Score 68.5;  DB 2;   Length 3144;
Best Local Similarity  28.0%;    Pred. No. 2e+02;
Matches   37;  Conservative  20;  Mismatches  36;  Indels  39;  Gaps   10;

Qy        19 SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE----DSSPDAARIR 70
             | ||:||::|.|| .  :.::|:||: ||:||::|  |   ||:||   || :|
Db      1354 SGGKGEIKSPSPDPASL---SSESERTATPQSLQGSNKSNIKNPEQKYLDFSFKAPKIA 1409

Qy        71 VKRYRQ------SMNN------FQGLRSEFGCRFG---TCTVQKLAHQIYQFTDKD----K 111
             : |:|       .||         |    |||   ||  | ||| :   :  |
Db      1410 LTLYNKTKGVTSLNDCGLTRIMFQDI---GCSLGLKNDGTVDGQAH-VAAFRIEDVRNIK 1465

Qy       112 DN----VAPRSK 119
             ||      :|:||
Db      1466 DNKHTELIPKSK 1477


Search completed: October 17, 2002, 15:22:40
Job time : 13.8078 secs
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OM protein - protein search, using sw model

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                GenCore version 5.1.3
        Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:         October 17, 2002, 15:20:12 ; Search time 21.5798 Seconds
                                             (without alignments)
                                             643.390 Million cell updates/sec

Title:          US-10-018-924-2_COPY_22_146
Perfect score:  655
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Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:     747574

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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   21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
   22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	185	22	AAB49697	Human adrenomeduli
2	655	100.0	185	22	AAB60344	Human adrenomeduli
3	611	93.3	188	22	AAB49698	Porcine adrenomedu
4	611	93.3	188	22	AAB60345	Porcine adrenomedu
5	458.5	70.0	185	22	AAB49699	Rat adrenomedulin
6	458.5	70.0	185	22	AAB60346	Rat adrenomedulin
7	384	58.6	97	21	AAG00251	Human secreted pro
8	299.5	45.7	120	22	AAB75122	UspA(1-57)-(A)-(GS
9	292	44.6	147	22	AAB75124	UspA(1-84)-(A)-(GS
10	291.5	44.5	120	22	AAB75123	UspA(1-56)-(DD)-(G
11	283	43.2	52	22	AAB75110	Human adrenomeduli
12	283	43.2	52	22	AAB91759	Adrenomedullin pep
13	283	43.2	52	22	AAE09818	Human adrenomedull
14	283	43.2	53	22	AAB75111	Glycine extended h
15	283	43.2	53	22	AAB75112	Glycine extended a
16	283	43.2	62	22	AAB75113	Linker peptide-adr
17	283	43.2	170	22	AAB75114	Thioredoxin-(GSGSG
18	239	36.5	50	22	AAB91763	Adrenomedullin pep
19	231	35.3	50	22	AAE09819	Rat adrenomedullin
20	227	34.7	52	22	AAB91765	Adrenomedullin pep
21	219.5	33.5	53	22	AAB91767	Adrenomedullin pep
22	196	29.9	40	22	AAB91768	Adrenomedullin pep
23	181.5	27.7	37	18	AAB91761	Adrenomedullin pep
24	163	24.9	31	22	AAW25160	Human preproadreno
25	163	24.9	31	22	AAB91762	Adrenomedullin pep
26	163	24.9	31	22	AAE09827	Human adrenomedull
27	107	16.3	20	18	AAW25161	Human proadrenomed
28	104	15.9	20	22	AAB91766	Adrenomedullin pep
29	97	14.8	20	22	AAB91769	Adrenomedullin pep
30	75	11.5	435	21	AAB07529	A mutant parathyro
31	75	11.5	446	21	AAY96983	Tethered PTH-1 rec
32	75	11.5	591	13	AAR27706	Rat bone PTH/PTHrP
33	75	11.5	591	17	AAR92277	Rat bone PTH/PTHrP
34	71	10.8	591	20	AAW73316	Parathyroid hormon
35	71	10.8	2224	17	AAW04254	Human Factor V. H
36	71	10.8	2224	17	AAY49564	Human lipoprotein
37	70.5	10.8	185	22	ABG05508	Novel human diagno
38	70	10.7	343	22	AAU62051	Propionibacterium
39	69	10.5	783	22	AAG91263	C glutamicum prote
40	68.5	10.5	401	22	AAM79810	Human protein SEQ
41	68.5	10.5	462	21	AAB18668	A human regulator
42	68.5	10.5	462	22	AAM78826	Human protein SEQ
43	68	10.4	515	22	ABG19073	Novel human diagno
44	68	10.4	651	22	ABG08359	Novel human diagno
45	68	10.4	944	22	ABG02404	Novel human diagno

ALIGNMENTS

```
RESULT 1
AAB49697
ID   AAB49697 standard; Protein; 185 AA.
XX
AC   AAB49697;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human adrenomedulin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedulin; urinary disorder; incontinence; human.
XX
OS   Homo sapiens.
XX
PN   WO200078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999; 99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29138.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedulin -
XX
PS   Claim 1; Page 26-27; 42pp; Japanese.
```

XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the human adrenomedullin protein, which is used in the
CC   composition of the invention.
XX
SQ   Sequence 185 AA;

Query Match   100.0%;   Score 655; DB 22; Length 185;
Best Local Similarity   100.0%; Pred. No. 1.8e-69;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141

Qy  121 SPQGY 125
        |||||
Db  142 SPQGY 146
```

RESULT 2
AAB60344
ID   AAB60344 standard; Protein; 185 AA.
XX
AC   AAB60344;
XX
DT   06-APR-2001 (first entry)
XX
DE   Human adrenomedullin precursor.
XX
KW   Human; adrenomedullin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obsteric; gynaecological.
XX
OS   Homo sapiens.
XX
PN   WO20078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999; 99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27228.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Claim 7; Page 37-38; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence

CC   represents human adrenomedullin precursor.
XX
SQ   Sequence 185 AA;

Query Match   100.0%;   Score 655; DB 22; Length 185;
Best Local Similarity   100.0%; Pred. No. 1.8e-69;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81

Qy   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141

Qy  121 SPQGY 125
        |||||
Db  142 SPQGY 146
```

RESULT 3
AAB49698
ID   AAB49698 standard; Protein; 188 AA.
XX
AC   AAB49698;
XX
DT   04-APR-2001 (first entry)
XX
DE   Porcine adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; procine.
XX
OS   Sus scrofa.
XX
PN   WO20078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999; 99JP-0177549.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29139.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedullin -
XX
PS   Disclosure; Page 31-33; 42pp; Japanese.
XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the porcine adrenomedullin protein, which is used in the
CC   composition of the invention.
XX
SQ   Sequence 188 AA;

Query Match   93.3%;   Score 611; DB 22; Length 188;
Best Local Similarity   91.2%; Pred. No. 3.1e-64;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

```
Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||::||:||||::
```

```
Db    22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81

Qy    61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
         | |||||||||||||||||||||||||||||||||||||||||||||||| |||||:||
Db    82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141

Qy   121 SPQGY 125
         |||||
Db   142 SPQGY 146
```

RESULT 4
AAB60345
```
ID   AAB60345 standard; Protein; 188 AA.
XX
AC   AAB60345;
XX
DT   06-APR-2001 (first entry)
XX
DE   Porcine adrenomedullin precursor.
XX
KW   Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Sus scrofa.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999; 99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27229.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Disclosure; Page 43-44; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents porcine adrenomedullin precursor.
XX
SQ   Sequence   188 AA;

Query Match     93.3%;  Score 611; DB 22;  Length 188;
Best Local Similarity   91.2%;  Pred. No. 3.1e-64;
Matches  114; Conservative   8; Mismatches   3; Indels   0; Gaps   0;

Qy     1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
         ||||||:|||||||||||||||||||||:|||||||||:||||||:|||||::||:||:
Db    22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81

Qy    61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
         | |||||||||||||||||||||||||||||||||||||||||||||||| |||||:||
Db    82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141

Qy   121 SPQGY 125
         |||||
```

```
Db   142 SPQGY 146
```

RESULT 5
AAB49699
```
ID   AAB49699 standard; Protein; 185 AA.
XX
AC   AAB49699;
XX
DT   04-APR-2001 (first entry)
XX
DE   Rat adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; rat.
XX
OS   Rattus norvegicus.
XX
PN   WO200078338-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999; 99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29140.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedullin -
XX
PS   Disclosure; Page 37-38; 42pp; Japanese.
XX
CC   This invention relates to a composition for promoting passive elongation
CC   of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC   uropathic activity. The composition can be used for promoting passive
CC   elongation of vesicle smooth muscles, this is useful for relieving
CC   urinary disorders such as impending urinary incontinence, reflex urinary
CC   incontinence and urinary incontinence with overflow. The present sequence
CC   represents the porcine adrenomedullin rat, which is used in the
CC   composition of the invention.
XX
SQ   Sequence   185 AA;

Query Match     70.0%;  Score 458.5; DB 22;  Length 185;
Best Local Similarity   72.8%;  Pred. No. 3.7e-46;
Matches   91; Conservative  10; Mismatches  21; Indels   3; Gaps   2;

Qy     1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
         ||||::||:|||||||||||||| |||:||||||:|::| :|:|:|:|| |:|: ::
Db    22 ARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80

Qy    61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
         |: ||||||||||||||||||||||||||||||||:||||||||||||||||: |||:||
Db    81 ASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDGMAPRNKI 138

Qy   121 SPQGY 125
         |||||
Db   139 SPQGY 143
```

RESULT 6
AAB60346
```
ID   AAB60346 standard; Protein; 185 AA.
XX
AC   AAB60346;
XX
DT   06-APR-2001 (first entry)
```

```
XX
DE   Rat adrenomedullin precursor.
XX
KW   Rat; adrenomedullin; precursor; bradykinin antagonist;
KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Rattus norvegicus.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999; 99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27230.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Disclosure; Page 48-49; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents rat adrenomedullin precursor.
XX
SQ   Sequence 185 AA;

Query Match             70.0%;  Score 453.5;  DB 22;  Length 185;
Best Local Similarity   72.8%;  Pred. No. 3.7e-46;
Matches   91;  Conservative   10;  Mismatches   21;  Indels    3;  Gaps    2;

Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
         |||:||||||||||||||||||||:||||||||||||| | :| | | :||
Db   22 ARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80

Qy   61 DSSPDAARIRVKRYRYRQSMNNFQGLRSFGCRFGICTVQKLAHQIYQFTDKDKDNVAPRSKI 120
         |: | ||||||||||||||||:||||||||||||||||||||||||||||| :|||:||
Db   81 ASTQSTAHIRVKRYRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKI 138

Qy  121 SPGGY 125
         |||||
Db  139 SPGGY 143


RESULT 7
AAG00251
ID   AAG00251 standard; Protein; 97 AA.
XX
AC   AAG00251;
XX
DT   06-OCT-2000 (first entry)
XX
DE   Human secreted protein, SEQ ID NO: 4332.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999; 99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   N-PSDB; AAC00257.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 13; SEQ ID '4332; 71pp + CD-ROM; English.
XX
CC   The present sequence is a polypeptide encoded by one of a large number
CC   of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC   were prepared from total human RNAs or polyA+ RNAs derived from 30
CC   different tissues. EST sequences usually correspond mainly to the 3'
CC   untranslated region (UTR) of the mRNA because they are often obtained
CC   from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC   isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC   those cases where longer cDNA sequences have been obtained, the full 5'
CC   UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC   ends and can therefore be used to obtain full length cDNAs and genomic
CC   DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC   chromosome mapping procedures. They are used to obtain upstream
CC   regulatory sequences and to design expression and secretion vectors.
XX
SQ   Sequence 97 AA;

Query Match             58.6%;  Score 384;  DB 21;  Length 97;
Best Local Similarity  100.0%;  Pred. No. 1.1e-37;
Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81

Qy   61 DSSPDAARIRVKRYR 75
         ||||||||||||||
Db   82 DSSPDAARIRVKRYR 96


RESULT 8
AAB75122
ID   AAB75122 standard; Protein; 120 AA.
XX
AC   AAB75122;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
```

```
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19864.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 68; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 120 AA;

Query Match             45.7%;  Score 299.5;  DB 22;  Length 120;
Best Local Similarity   64.7%;  Pred. No. 1.5e-27;
Matches   66;  Conservative   3;  Mismatches  12;  Indels  21;  Gaps  4;

Qy  24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
        ::  | : ||| ||     |      ||:   |      ||    ||||||||||
Db  39 DVNYSDLY-TGLIDVNLG-------DMAGS-----EYRQSMNNFQG 77

Qy  84 LRSFGCRRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
        |||||||||||||||||||||||||||||||||||||||||||
Db  78 LRSFGCRRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119


RESULT 9
AAB75124
ID   AAB75124 standard; Protein; 147 AA.
XX
AC   AAB75124;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19866.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
```

```
XX
PS   Claim 17; Page 71; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 147 AA;

Query Match             44.6%;  Score 292;  DB 22;  Length 147;
Best Local Similarity   57.0%;  Pred. No. 1.5e-26;
Matches   65;  Conservative   6;  Mismatches  25;  Indels  18;  Gaps  3;

Qy  24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS-----------SPDAARIRV 71
        ::  | : ||| ||     |      ||    |      |      ||
Db  39 DVNYSDLY-TGLIDVNLGDMQKRISEETHHALTELSTNAGYPITETLAGSGSGDAF---- 93

Qy  72 KRYRQSMNNFQGLRSFGCRRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94 -EYRQSMNNFQGLRSFGCRRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 10
AAB75123
ID   AAB75123 standard; Protein; 120 AA.
XX
AC   AAB75123;
XX
DT   31-JUL-2001 (first entry)
XX
DE   UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19855.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 69-70; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
```

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CC   exemplification of the present invention.
XX
SQ   Sequence   120 AA;

Query Match   44.5%; Score 291.5; DB 22; Length 120;
Best Local Similarity   63.7%; Pred. No. 1.3e-26;
Matches   65; Conservative   3; Mismatches 13; Indels 21; Gaps   4;

Qy   24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
          :: |--|:|| | : | : |: || | ||||||||
Db   39 DVNYSDLY-TGLIDVNLG-------------DDDGS------GSGDAF-----EYRQSMNNFQG 77

Qy   84 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          ||||||||||||||||||||||||||||||||||||||||||
Db   78 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119

RESULT 11
AAB75110
ID   AAB75110 standard; Protein; 52 AA.
XX
AC   AAB75110;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Human adrenomedullin (AM) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999; 99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19806.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 45; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   adrenomedullin precursor using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   52 AA;

Query Match   43.2%; Score 283; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.5e-26;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 12
AAB91759
ID   AAB91759 standard; Peptide; 52 AA.
XX
AC   AAB91759;
XX
DT   22-JUN-2001 (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999; 99US-0134406.
PR   10-SEP-1999; 99US-0153406.
PR   15-OCT-1999; 99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 498; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   52 AA;

Query Match   43.2%; Score 283; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.5e-26;
Matches   52; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 13
AAE09818
ID   AAE09818 standard; peptide; 52 AA.
XX

AC   AAE09818;
XX
DT   29-NOV-2001 (first entry)
XX
DE   Human adrenomedullin peptide #1.
XX
KW   Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW   CGRP-receptor identification; adrenomedullin.
XX
OS   Homo sapiens.
XX
PN   US626474-B1.
XX
PD   31-JUL-2001.
XX
PF   30-APR-1998;   98US-0070504.
XX
PR   30-APR-1998;   98US-0070504.
XX
PA   (UVCR-) UNIV CREIGHTON.
XX
PI   Smith DD, Saha S, Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related
PT   peptide receptor activity -
XX
PS   Claim 5; Column 25-26; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide
CC   calcitonin gene related peptide (CGRP) and other members of the
CC   CGRP superfamily. The invention also relates to amino the terminal
CC   modifications of peptides to improve their ability to bind to a
CC   member of the CGRP-receptor super-family. CGRP antagonists are
CC   used for inhibiting CGRP activity which can be used in vitro e.g.
CC   in assays to identify and/or isolate CGRP receptors or with intact
CC   cells either in vitro or in vivo to inhibit the effect of CGRP
CC   binding to its receptor. The present sequence is human
CC   adrenomedullin peptide.
XX
SQ   Sequence 52 AA;

Query Match   43.2%;   Score 283; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.5e-26;
Matches   52; Conservative   0; Mismatches   0;   Indels   0; Gaps   0;

Qy   74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 14
AAB75111
ID   AAB75111 standard; Protein; 53 AA.
XX
AC   AAB75111;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Glycine extended human adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX

PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19807.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Example 1; Page 46; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 53 AA;

Query Match   43.2%;   Score 283; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches   52; Conservative   0; Mismatches   0;   Indels   0; Gaps   0;

Qy   74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 15
AAB75112
ID   AAB75112 standard; Protein; 53 AA.
XX
AC   AAB75112;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Glycine extended adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19808.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 47; 75pp; Japanese.
XX

```
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ       Sequence    53 AA;

Query Match         43.2%;   Score 283;  DB 22;   Length 53;
Best Local Similarity  100.0%;  Pred. No. 4.6e-26;
Matches   52;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


Search completed: October 17, 2002, 15:21:13
Job time : 22.5798 secs
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                    GenCore version 5.1.3
              Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        October 17, 2002, 14:45:21 ; Search time 2.39401 Seconds
                                           (without alignments)
                                 646.939 Million cell updates/sec

Title:      US-10-018-924-2_COPY_107_146
Perfect score: 219
Sequence:   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched:   105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:    105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SwissProt_40:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES
                %
Result          Query
No.    Score   Match  Length DB  ID            Description
-----  -----   -----  ------ --  -----------   -----------
 1     219     100.0   185    1  ADML_HUMAN    P35318 homo sapien
 2     213     97.3    188    1  ADML_PIG      P53366 sus scrofa
 3     208     95.0    188    1  ADML_CANFA    O77559 canis famil
 4     202     92.2    188    1  ADML_BOVIN    O62827 bos taurus
 5     196     89.5    185    1  ADML_RAT      P43145 rattus norv
 6     187     85.4    184    1  ADML_MOUSE    P97297 mus musculu
 7     61      27.9    1541   1  MRP2_RAT      Q63120 rattus norv
 8     59      26.9    1545   1  MRP2_HUMAN    Q92887 homo sapien
 9     55      25.1    1564   1  MRP2_RABIT    Q28689 oryctolagus
10     54.5    24.9    436    1  SLS6_BRAOL    P07761 brassica ol
11     51      23.3    180    1  VG48_BPMU     O9tIvl bacteriopha
12     51      23.3    1325   1  MRP4_HUMAN    O15439 homo sapien
13     50.5    23.1    459    1  G33_RAT       P05432 rattus norv
14     50.5    23.1    532    1  TYRO_RANNI    Q04604 rana nigrom
15     49.5    22.6    322    1  Y4KA_RHISN    P55521 rhizobium s
16     49      22.4    435    1  SLS2_BRAOA    P22553 brassica ol
17     49      22.4    941    1  DNAB_RHOMR    O30477 rhodothermu
18     49      22.4    1527   1  MRP3_HUMAN    O15438 homo sapien
19     48.5    22.1    465    1  INXB_CAEEL    Q23157 caenorhabdi
20     48.5    22.1    960    1  LI36_CAEEL    P34427 caenorhabdi
21     48      21.9    328    1  ZIPA_YERPE    P58492 yersinia pe
22     48      21.9    396    1  PPAS_XENLA    P37233 xenopus lae
23     48      21.9    425    1  SYH_METTH     O26346 methanobact
24     48      21.9    496    1  NMT1_HUMAN    P30419 homo sapien
25     48      21.9    496    1  NMT1_MOUSE    O70310 mus musculu
26     48      21.9    497    1  NMT1_BOVIN    P31717 bos taurus
27     48      21.9    672    1  KPCA_BOVIN    P04409 bos taurus
28     48      21.9    672    1  KPCA_HUMAN    P17252 homo sapien
29     48      21.9    672    1  KPCA_MOUSE    P20444 mus musculu
30     48      21.9    672    1  KPCA_RABIT    P10102 oryctolagus
31     48      21.9    672    1  KPCA_RAT      P05696 rattus norv
32     48      21.9    689    1  UVRA_PSELE    P52087 pseudomonas
33     48      21.9    1163   1  AT5C_HUMAN    O60312 homo sapien
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34     48      21.9   1252   1  RPOB_CHLMU    P56869 chlamydia m
35     48      21.9   1252   1  RPOB_CHLPN    Q9za0 chlamydia p
36     48      21.9   1252   1  RPOB_CHLTR    O84317 chlamydia t
37     48      21.9   1268   1  VGLN_HUMAN    O00341 homo sapien
38     47.5    21.7    144   1  YHP5_YEAST    P38808 saccharomyc
39     47.5    21.7    438   1  PRI1_DROME    Q24317 drosophila
40     47      21.5    273   1  TYRO_COTJA    Q08410 coturnix co
41     47      21.5    423   1  RECA_MYCFV    Q9f415 mycobacteri
42     47      21.5    545   1  FLIF_BUCAI    P57175 buchnera ap
43     47      21.5   1477   1  YOR1_YEAST    P53049 saccharomyc
44     47      21.5   1822   1  ITB4_HUMAN    P16144 homo sapien
45     46.5    21.2     76   1  RS18_NEIMA    O07815 neisseria m
```

ALIGNMENTS

```
RESULT 1
ADML_HUMAN
ID   ADML_HUMAN       STANDARD;      PRT;    185 AA.
AC   P35318;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93343928; PubMed=7688224;
RA   Kitamura K., Sakata J., Kangawa K., Matsuo H., Matsuo H., Eto T.;
RT   "Cloning and characterization of cDNA encoding a precursor for human
RT   adrenomedullin.";
RL   Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94354869; PubMed=8074714;
RA   Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA   Kitamura K., Eto T., Matsuo H.;
RT   "Genomic structure of human adrenomedullin gene.";
RL   Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN   [3]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=9249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [4]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445;
RA   Champion H.C. Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
CC       PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
CC       KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
```

CC   INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC   PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC   INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC   AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
CC   ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC   VESSELS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
CC   ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC   TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ---

DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JN0476; JN0476.
DR   PIR; JN0684; JN0684.
DR   PIR; JC2351; JC2351.
DR   MIM; 103275; -.
DR   InterPro; IPR001710; Adrenomedullin; 1.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92
FT   PEPTIDE   95   146   ADRENOMEDULLIN.
FT   PROPEP   148   185   PREPROAM C-TERMINAL FRAGMENT.
FT   DISULFID   110   115
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;

Query Match   100.0%; Score 219; DB 1; Length 185;
Best Local Similarity   100.0%; Pred. No. 2.7e-23;
Matches   40; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
             ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 2
ADML_PIG
ID   ADML_PIG   STANDARD;   PRT;   188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM OR AM.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning
RT   of cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]

RP   SEQUENCE OF 22-41.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin
RT   N-terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC   AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC   KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   ---

DR   EMBL; D14875; BAA03590.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL   1   21
FT   PEPTIDE   22   41   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP   45   92
FT   PEPTIDE   95   146   ADRENOMEDULLIN.
FT   PROPEP   153   188   PREPROAM C-TERMINAL FRAGMENT (BY
FT   SIMILARITY).
FT   DISULFID   110   115   BY SIMILARITY.
FT   MOD_RES   41   41   AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT   MOD_RES   146   146   AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   188 AA; 20893 MW; 71749460F5660A61 CRC64;

Query Match   97.3%; Score 213; DB 1; Length 188;
Best Local Similarity   97.5%; Pred. No. 1.9e-22;
Matches   39; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
             ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 3
ADML_CANFA
ID   ADML_CANFA   STANDARD;   PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99007040; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).

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CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   -------------------------------------------------------------------
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CC   -------------------------------------------------------------------
DR   EMBL; AF045773; AAD05423.1; -.
DR   EMBL; U96127; AAD09957.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   CONFLICT    130    130       N -> K (IN REF. 2).
SQ   SEQUENCE    188 AA;   20929 MW;   809D6A64F98F5578 CRC64;

Query Match              95.0%;   Score 208; DB 1; Length 188;
Best Local Similarity    95.0%;          Pred. No. 9.3e-22;
Matches     38;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||| |||||||||||||||||||||
Db    107 SFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146

RESULT 4
ADML_BOVIN
ID   ADML_BOVIN      STANDARD;       PRT;    188 AA.
AC   O62827;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC       CIRCULATION CONTROL (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    146       ADRENOMEDULLIN.
FT   PROPEP      148    188       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    110    115       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     146    146       AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
SQ   SEQUENCE    188 AA;   20981 MW;   3002E79AB3B6612C CRC64;

Query Match              92.2%;   Score 202; DB 1; Length 188;
Best Local Similarity    92.5%;          Pred. No. 6.4e-21;
Matches     37;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||  |||||||||||||||||||||
Db    107 SFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146

RESULT 5
ADML_RAT
ID   ADML_RAT       STANDARD;        PRT;    185 AA.
AC   P43145;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX   MEDLINE=93384621; PubMed=7690563;
RA   Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA   Matsuo H., Eto T.;
RT   "Molecular cloning and biological activities of rat adrenomedullin, a
RT   hypotensive peptide.";
RL   Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96102137; PubMed=8524787;
RA   Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA   Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT   "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT   its role in exacerbating focal brain ischemic damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC       HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC   -------------------------------------------------------------------
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CC   -------------------------------------------------------------------------
DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     91       BY SIMILARITY.
FT   PEPTIDE      94    143       ADRENOMEDULLIN.
FT   PROPEP      149    185       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    107    112       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     143    143       AMIDATION (G-144 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
SQ   SEQUENCE    185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;
Query Match             89.5%;  Score 196; DB 1; Length 185;
Best Local Similarity   87.5%;  Pred. No. 4.3e-20;
Matches    35;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
             |||||||||||||||||||||:||:|||:||||||||||||
Db       104 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143

RESULT 6
ADML_MOUSE
ID   ADML_MOUSE     STANDARD;      PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   ADM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RA   Yotsumoto S., Ko M.S.H.;
RT   "Expression of mouse adrenomedullin gene in trophoblastic giant
RT   cells at the implantation site.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC       AGENTS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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CC   -------------------------------------------------------------------------
DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   PEPTIDE      22     41       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT   PROPEP       45     92       BY SIMILARITY.
FT   PEPTIDE      95    144       ADRENOMEDULLIN.
FT   PROPEP      151    184       PREPROAM C-TERMINAL FRAGMENT (BY
FT                                SIMILARITY).
FT   DISULFID    108    113       BY SIMILARITY.
FT   MOD_RES      41     41       AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   MOD_RES     144    144       AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT                                (BY SIMILARITY).
FT   CONFLICT    173    173       A -> G (IN REF. 2).
SQ   SEQUENCE    184 AA;  20764 MW;  C88C99045A79C898 CRC64;
Query Match             85.4%;  Score 187; DB 1; Length 184;
Best Local Similarity   85.0%;  Pred. No. 7.5e-19;
Matches    34;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
             ||:|||||||:|||||||||:|||||||:||||||||||||
Db       105 SNGCRFGTCTFQKLAHQIYQLTDKDKDGMAPRNKISPQGY 144

RESULT 7
MRP2_RAT
ID   MRP2_RAT       STANDARD;      PRT;  1541 AA.
AC   Q63120; Q63145;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 1 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein).
GN   ABCC2 OR CMOAT OR MRP2 OR CMRP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=96180672; PubMed=8599091;
RA   Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M.,
RA   Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
RT   "Congenital jaundice in rats with a mutation in a multidrug
RT   resistance-associated protein gene.";
RL   Science 271:1126-1128(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RX   MEDLINE=96279006; PubMed=8662992;
RA   Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
RA   Keppler D.;
RT   "cDNA cloning of the hepatocyte canalicular isoform of the multidrug
RT   resistance protein, cMrP, reveals a novel conjugate export pump
RT   deficient in hyperbilirrubinemic mutant rats.";
RL   J. Biol. Chem. 271:15091-15098(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA   Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Sugiyama Y.;
RT   "Expression of the putative ATP-binding cassette region, homologous to
RT   that in multidrug resistance associated protein (MRP), is hereditarily
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RT   defective in Eisai hyperbilirubinemic rats (EHBR).";
RL   Int. Hepatol. Commun. 292:292-299(1996).
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC       ANIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
CC   -!- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED
CC       HYPERBILIRUBINEMIA (EHBR).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; L49379; AAC42087.1; -.
DR   EMBL; X96393; CAA65257.1; -.
DR   EMBL; D86086; BAA13016.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT   DOMAIN          1     26    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM       27     47    1 (BY SIMILARITY).
FT   DOMAIN         48     67    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM       68     88    2 (BY SIMILARITY).
FT   DOMAIN         89     92    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM       93    113    3 (BY SIMILARITY).
FT   DOMAIN        114    125    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM      126    146    4 (BY SIMILARITY).
FT   DOMAIN        147    164    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM      165    185    5 (BY SIMILARITY).
FT   DOMAIN        186    309    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM      310    330    6 (BY SIMILARITY).
FT   DOMAIN        331    356    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM      357    377    7 (BY SIMILARITY).
FT   DOMAIN        378    433    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM      434    454    8 (BY SIMILARITY).
FT   DOMAIN        455    457    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM      458    478    9 (BY SIMILARITY).
FT   DOMAIN        479    540    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM      541    561    10 (BY SIMILARITY).
FT   DOMAIN        562    583    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM      584    604    11 (BY SIMILARITY).
FT   DOMAIN        605    967    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM      968    988    12 (BY SIMILARITY).
FT   DOMAIN        989   1029    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     1030   1050    13 (BY SIMILARITY).
FT   DOMAIN       1051   1093    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     1094   1114    14 (BY SIMILARITY).
FT   DOMAIN       1115   1115    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     1116   1136    15 (BY SIMILARITY).
FT   DOMAIN       1137   1207    CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     1208   1228    16 (BY SIMILARITY).
FT   DOMAIN       1229   1230    EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     1231   1251    17 (BY SIMILARITY).
FT   DOMAIN       1252   1541    CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND       667    674    ATP (POTENTIAL).
FT   NP_BIND      1330   1337    ATP (POTENTIAL).
FT   CARBOHYD        6      6    N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     1007   1007    N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     1010   1010    N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     1011   1011    N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CONFLICT      420    420    M -> V (IN REF. 3).
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SQ   SEQUENCE   1541 AA;  173383 MW;  D5FB5571BFDB39 CRC64;

Query Match      27.9%;   Score 61;  DB 1;  Length 1541;
Best Local Similarity  38.2%;   Pred. No. 2.2;
Matches 13;  Conservative 4;  Mismatches 17;  Indels 0;  Gaps 0;

Qy    6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG   39
         | ||| :||:||:::  |  |||  |    ||
Db 1479 FSQCTVITIAHRLHTIMDSDKIMVLDNGKIVEYG  1512


RESULT 8
MRP2_HUMAN
ID   MRP2_HUMAN     STANDARD;      PRT;   1545 AA.
AC   Q92887; Q99663; Q92798; Q14022; Q92500; Q9UMS2;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 1 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein).
GN   ABCC2 OR CMOAT1 OR CMOAT OR MRP2 OR CMRP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96390592; PubMed=8797578;
RA   Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M.,
RA   Kagotani K., Okumura K., Akiyama S., Kuwano M.;
RT   "A human canalicular multispecific organic anion transporter (cMOAT)
RT   gene is overexpressed in cisplatin-resistant human cancer cell lines
RT   with decreased drug accumulation.";
RL   Cancer Res. 56:4124-4129(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
RA   Baas F., Borst P.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96279006; PubMed=8662992;
RA   Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
RA   Keppler D.;
RT   "cDNA cloning of the hepatocyte canalicular isoform of the multidrug
RT   resistance protein, cMrp, reveals a novel conjugate export pump
RT   deficient in hyperbilirubinemic mutant rats.";
RL   J. Biol. Chem. 271:15091-15098(1996).
RN   [4]
RP   REVISIONS.
RA   Keppler D.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99395001; PubMed=10464142;
RA   Tsujii H., Koenig J., Rost D., Stoeckel B., Leuschner U., Keppler D.;
RT   "Exon-intron organization of the human multidrug-resistance protein 2
RT   (MRP2) gene mutated in Dubin-Johnson syndrome.";
RL   Gastroenterology 117:653-660(1999).
RN   [6]
RP   VARIANT DJS TRP-768.
RX   MEDLINE=98087571; PubMed=9425227;
RA   Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
RA   Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
RT   "Mutations in the canalicular multispecific organic anion transporter
RT   (cMOAT) gene, a novel ABC transporter, in patients with
RT   hyperbilirubinemia II/Dubin-Johnson syndrome.";
RL   Hum. Mol. Genet. 7:203-207(1998).
RN   [7]
RP   VARIANTS DJS TRP-768 AND ARG-1382.
RX   MEDLINE=99162196; PubMed=10053008;
RA   Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y.,
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RA   Adachi Y., Sakisaka S., Kuwano M.;
RT   "Genomic structure of the canalicular multispecific organic anion-
RT   transporter gene (MRP2/cMOAT) and mutations in the ATP-binding-
RT   cassette region in Dubin-Johnson syndrome.";
RL   Am. J. Hum. Genet. 64:739-746(1999).
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC       ANIONS. MAY FUNCTION AS A CELLULAR CISPLATIN TRANSPORTER.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
CC   -!- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF DUBIN-JOHNSON SYNDROME
CC       (DJS), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONJUGATED
CC       HYPERBILIRUBINEMIA, AN INCREASE IN THE URINARY EXCRETION OF
CC       COPROPORPHYRIN ISOMER I, DEPOSITION OF MELANIN-LIKE PIGMENT IN
CC       HEPATOCYTES, AND PROLONGED RETENTION OF SULFOBROMOPHTHALEIN, BUT
CC       OTHERWISE NORMAL LIVER FUNCTION.
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U63970; AAB39892.1; -.
DR   EMBL; U49248; AAB09422.1; -.
DR   EMBL; X96395; CAA65259.2; -.
DR   EMBL; AJ132244; CAB45309.1; -.
DR   EMBL; AJ132287; CAB45309.1; JOINED.
DR   EMBL; AJ245625; CAB45309.1; JOINED.
DR   EMBL; AJ132288; CAB45309.1; JOINED.
DR   EMBL; AJ132289; CAB45309.1; JOINED.
DR   EMBL; AJ132290; CAB45309.1; JOINED.
DR   EMBL; AJ132291; CAB45309.1; JOINED.
DR   EMBL; AJ132292; CAB45309.1; JOINED.
DR   EMBL; AJ132293; CAB45309.1; JOINED.
DR   EMBL; AJ132294; CAB45309.1; JOINED.
DR   EMBL; AJ132295; CAB45309.1; JOINED.
DR   EMBL; AJ132296; CAB45309.1; JOINED.
DR   EMBL; AJ132297; CAB45309.1; JOINED.
DR   EMBL; AJ132298; CAB45309.1; JOINED.
DR   EMBL; AJ132299; CAB45309.1; JOINED.
DR   EMBL; AJ132300; CAB45309.1; JOINED.
DR   EMBL; AJ132301; CAB45309.1; JOINED.
DR   EMBL; AJ132302; CAB45309.1; JOINED.
DR   EMBL; AJ132303; CAB45309.1; JOINED.
DR   EMBL; AJ132311; CAB45309.1; JOINED.
DR   EMBL; AJ245626; CAB45309.1; JOINED.
DR   EMBL; AJ132312; CAB45309.1; JOINED.
DR   EMBL; AJ132304; CAB45309.1; JOINED.
DR   EMBL; AJ132305; CAB45309.1; JOINED.
DR   EMBL; AJ132306; CAB45309.1; JOINED.
DR   EMBL; AJ132313; CAB45309.1; JOINED.
DR   EMBL; AJ132307; CAB45309.1; JOINED.
DR   EMBL; AJ132308; CAB45309.1; JOINED.
DR   EMBL; AJ245627; CAB45309.1; JOINED.
DR   EMBL; AJ132309; CAB45309.1; JOINED.
DR   EMBL; AJ132310; CAB45309.1; JOINED.
DR   EMBL; AJ132314; CAB45309.1; JOINED.
DR   HSSP; P13569; 1NBD.
DR   MIM; 601107; -.
DR   MIM; 237500; -.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
KW   Disease mutation.

FT   DOMAIN        1     27   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     28     48   1 (BY SIMILARITY).
FT   DOMAIN       49     68   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM     69     89   2 (BY SIMILARITY).
FT   DOMAIN       90     93   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM     94    114   3 (BY SIMILARITY).
FT   DOMAIN      115    126   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    127    147   4 (BY SIMILARITY).
FT   DOMAIN      148    165   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    166    186   5 (BY SIMILARITY).
FT   DOMAIN      187    313   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    314    334   6 (BY SIMILARITY).
FT   DOMAIN      335    360   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    361    381   7 (BY SIMILARITY).
FT   DOMAIN      382    437   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    438    458   8 (BY SIMILARITY).
FT   DOMAIN      459    461   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    462    482   9 (BY SIMILARITY).
FT   DOMAIN      483    544   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    545    565   10 (BY SIMILARITY).
FT   DOMAIN      566    587   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM    588    608   11 (BY SIMILARITY).
FT   DOMAIN      609    971   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM    972    992   12 (BY SIMILARITY).
FT   DOMAIN      993   1033   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1034   1054   13 (BY SIMILARITY).
FT   DOMAIN     1055   1097   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1098   1118   14 (BY SIMILARITY).
FT   DOMAIN     1119   1119   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1120   1140   15 (BY SIMILARITY).
FT   DOMAIN     1141   1211   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1212   1232   16 (BY SIMILARITY).
FT   DOMAIN     1233   1234   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1235   1255   17 (BY SIMILARITY).
FT   DOMAIN     1256   1545   CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND     671    678   ATP (POTENTIAL).
FT   NP_BIND    1334   1341   ATP (POTENTIAL).
FT   CARBOHYD      7      7   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     12     12   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1011   1011   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     768    768   R -> W (IN DJS).
FT                            /FTId=VAR_000099.
FT   VARIANT    1382   1382   Q -> R (IN DJS).
FT                            /FTId=VAR_010756.
FT   CONFLICT   1188   1188   V -> E (IN REF. 2).
FT   CONFLICT   1430   1430   V -> G (IN REF. 5).
FT   CONFLICT   1515   1515   C -> Y (IN REF. 2).
SQ   SEQUENCE   1545 AA;  174190 MW;  EA12668A4DD0F391 CRC64;

Query Match             26.9%;  Score 59;  DB 1;  Length 1545;
Best Local Similarity   37.8%;  Pred. No. 4.2;
Matches  14;  Conservative   5;  Mismatches  14;  Indels  4;  Gaps  1;

Qy       6  FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
            | ||| :||::: :||| | |||  |  |  ||:
Db    1483  FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSPE 1519


RESULT 9
ID   MRP2_RABIT      STANDARD;      PRT;   1564 AA.
AC   Q28689;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Canalicular multispecific organic anion transporter 1 (Multidrug
DE   resistance-associated protein 2) (Canalicular multidrug resistance
DE   protein) (Epithelial basolateral chloride conductance regulator).
GN   ABCC2 OR MRP2 OR EBCR.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
```

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ileum;
RX   MEDLINE=96224297; PubMed=8643587;
RA   van Kuijck M.A., van Aubel R.A.M.H., Busch A.E., Lang F.,
RA   Russel F.G.M., Bindels R.J.M., van Os C.H., Deen P.M.T.;
RT   "Molecular cloning and expression of a cyclic AMP-activated chloride
RT   conductance regulator: a novel ATP-binding cassette transporter.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=98279125; PubMed=9614209;
RA   van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
RA   van Os C.H., Russel F.G.M.;
RT   "Adenosine triphosphate-dependent transport of anionic conjugates by
RT   the rabbit multidrug resistance-associated protein Mrp2 expressed in
RT   insect cells.";
RL   Mol. Pharmacol. 53:1062-1067(1998).
CC   -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
CC   ANIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SMALL
CC   INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC   --

DR   EMBL; Z49144; CAA89004.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR001140; ABC_transporter_tmem.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT   DOMAIN   1   27   (BY SIMILARITY).
FT   TRANSMEM   28   48   1 (BY SIMILARITY).
FT   DOMAIN   49   68   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   69   89   2 (BY SIMILARITY).
FT   DOMAIN   90   93   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   94   114   3 (BY SIMILARITY).
FT   DOMAIN   115   126   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   127   147   4 (BY SIMILARITY).
FT   TRANSMEM   148   165   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN   166   186   5 (BY SIMILARITY).
FT   TRANSMEM   187   311   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   312   332   6 (BY SIMILARITY).
FT   TRANSMEM   333   358   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN   359   379   7 (BY SIMILARITY).
FT   TRANSMEM   380   435   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   436   456   8 (BY SIMILARITY).
FT   TRANSMEM   457   459   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN   460   480   9 (BY SIMILARITY).
FT   TRANSMEM   481   542   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   543   563   10 (BY SIMILARITY).
FT   TRANSMEM   564   585   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN   586   606   11 (BY SIMILARITY).
FT   TRANSMEM   607   969   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   970   990   12 (BY SIMILARITY).
FT   TRANSMEM   991   1031   EXTRACELLULAR (BY SIMILARITY).
FT   DOMAIN   1032   1052   13 (BY SIMILARITY).
FT   TRANSMEM   1053   1095   CYTOPLASMIC (BY SIMILARITY).
FT   DOMAIN   1096   1116   14 (BY SIMILARITY).
FT   DOMAIN   1117   EXTRACELLULAR (BY SIMILARITY).

FT   TRANSMEM   1118   1138   15 (BY SIMILARITY).
FT   DOMAIN - 1139   1209   CYTOPLASMIC (BY SIMILARITY).
FT   TRANSMEM   1210   1230   16 (BY SIMILARITY).
FT   DOMAIN   1231   1232   EXTRACELLULAR (BY SIMILARITY).
FT   TRANSMEM   1233   1253   17 (BY SIMILARITY).
FT   DOMAIN   1254   1543   CYTOPLASMIC (BY SIMILARITY).
FT   NP_BIND   669   676   ATP (POTENTIAL).
FT   NP_BIND   1332   1339   ATP (POTENTIAL).
FT   CARBOHYD   7   7   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   12   12   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   1009   1009   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   1564 AA; 175542 MW; D8FBF5AC8FE45873 CRC64;

Query Match   25.1%; Score 55; DB 1; Length 1564;
Best Local Similarity   35.38%;
Matches   12; Conservative   4; Mismatches   18; Indels   0; Gaps   0;

Qy   6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 39
              | |||| ||:: || ::: || ||| |
Db   1481 FSHCTVITIAHRLHTIMDSDKIMVLDNGNIVEYG 1514

RESULT 10
SLS6_BRAOL
ID   SLS6_BRAOL   STANDARD;   PRT;   436 AA.
AC   P07761;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   S-locus-specific glycoprotein S6 precursor (SLSG-6).
GN   SLSG.
OS   Brassica oleracea (Cauliflower).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3712;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
RT   "Amino-acid sequence of glycoproteins encoded by three alleles of the
RT   S locus of Brassica oleracea.";
RL   Nature 326:617-619(1987).
RN   [2]
RP   SEQUENCE OF 22-435 FROM N.A.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RT   "A cDNA clone encoding an s-locus-specific glycoprotein from Brassica
RT   oleracea.";
RL   Nature 318:263-267(1985).
RN   [3]
RP   ERRATUM.
RA   Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RL   Nature 326:523-523(1987).
CC   -!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC   (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
CC   -!- TISSUE SPECIFICITY: STIGMA.
CC   -!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
CC   B.OLERACEA.
CC   -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
CC   KINASE RECEPTOR (ZMPK1).
CC   --

DR   EMBL; Y00268; CAA68375.1; -.
DR   EMBL; X03170; CAA26934.1; ALT_INIT.
DR   PIR; A27827; A27827.
DR   InterPro; IPR001480; B_lectin.
DR   InterPro; IPR003609; Pan_app.

```
DR   InterPro; IPR000858; S_locus_glycop.
DR   Pfam; PF01453; Agglutinin; 1.
DR   Pfam; PF00954; S_locus_glycop; 1.
DR   SMART; SM00108; B_lectin; 1.
DR   SMART; SM00473; PAN_AP; 1.
KW   Self-incompatibility; Glycoprotein; Polymorphism; Signal.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN        32    436       S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
FT   CARBOHYD     46     46       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     64     64       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    121    121       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    245    245       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    261    261       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    390    390       N-LINKED (GLCNAC...)   (POTENTIAL).
SQ   SEQUENCE    436 AA;  49779 MW;  E2332635B8B5A515 CRC64;

Query Match             24.9%;  Score 54.5;  DB 1;  Length 436;
Best Local Similarity   28.6%;  Pred. No. 4.8;
Matches   14;  Conservative   10;  Mismatches   14;  Indels   11;  Gaps    2;

Qy      3 GCRF-GTCTVQKLAHQIYQFTDKDKD--------NVAPRSKISPQGY 40
            | ||  |||::|| :|  ||     ::    :| :|  :| :||
Db    227 GVRFSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275

RESULT 11
VG48_BPMU
ID   VG48_BPMU    STANDARD;    PRT;    180 AA.
AC   Q9T1V1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein gp48.
GN   48.
OS   Bacteriophage Mu.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX   NCBI_TaxID=10677;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Morgan G., Hatfull G., Hendrix R.;
RT   "Genome of bacteriophage Mu and comparison with the Haemophilus
RT   influenzae Mu-like prophage FluMu.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: SOME, TO H.INFLUENZAE HI1521 AND SOME, TO E.COLI YMFQ.
CC   ---------------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF083977; AAF01126.1; -.
SQ   SEQUENCE    180 AA;  20468 MW;  3045A6C185B48BF9 CRC64;

Query Match             23.3%;  Score 51;  DB 1;  Length 180;
Best Local Similarity   50.0%;  Pred. No. 5.8;
Matches   11;  Conservative    3;  Mismatches    3;  Indels    6;  Gaps    2;

Qy      9 CTVQKL--AHQIYQFTDKDKDN 28
           | :|| ||||:|  |
Db    159 CLLEKYKPAHQIYKFVHDGDN 180

RESULT 12
MRP4_HUMAN
ID   MRP4_HUMAN   STANDARD;    PRT;    1325 AA.
AC   O15439; Q9Y6J2;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
```

```
DE   Multidrug resistance-associated protein 4 (MRP/cMOAT-related ABC
DE   transporter) (MOAT-B).
GN   ABCC4 OR MRP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98324262; PubMed=9661885;
RA   Lee K., Belinsky M.G., Bell D.W., Testa J.R., Kruh G.D.;
RT   "Isolation of MOAT-B, a widely expressed multidrug resistance-
RT   associated protein/canalicular multispecific organic anion
RT   transporter-related transporter.";
RL   Cancer Res. 58:2741-2747(1998).
RN   [2]
RP   SEQUENCE OF 1155-1316 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97413640; PubMed=9270026;
RA   Kool M., de Haas M., Scheffer G.L., Scheper R.J., van Eijk M.J.,
RA   Juijn J.A., Baas F., Borst P.;
RT   "Analysis of expression of cMOAT (MRP2), MRP3, MRP4, and MRP5,
RT   homologues of the multidrug resistance-associated protein gene
RT   (MRP1) in human cancer cell lines.";
RL   Cancer Res. 57:3537-3547(1997).
CC   -!- FUNCTION: MAY BE AN ORGANIC ANION PUMP RELEVANT TO CELLULAR
CC       DETOXIFICATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH PARTICULARLY HIGH
CC       LEVELS IN PROSTATE, BUT IS BARELY DETECTABLE IN LIVER.
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF071202; AAC27076.1; -.
DR   EMBL; U83660; AAB71757.1; -.
DR   HSSP; P13569; 1NBD.
DR   MIM; 605250; -.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR003439; ABC_transporter.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00005; ABC_tran; 2.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT   TRANSMEM     93    113       POTENTIAL.
FT   TRANSMEM    136    156       POTENTIAL.
FT   TRANSMEM    207    227       POTENTIAL.
FT   TRANSMEM    228    248       POTENTIAL.
FT   TRANSMEM    328    348       POTENTIAL.
FT   TRANSMEM    351    371       POTENTIAL.
FT   TRANSMEM    440    460       POTENTIAL.
FT   TRANSMEM    710    730       POTENTIAL.
FT   TRANSMEM    771    791       POTENTIAL.
FT   TRANSMEM    836    856       POTENTIAL.
FT   TRANSMEM    858    878       POTENTIAL.
FT   TRANSMEM    954    974       POTENTIAL.
FT   TRANSMEM    977    997       POTENTIAL.
FT   TRANSMEM   1038   1058       POTENTIAL.
FT   NP_BIND     445    452       ATP (POTENTIAL).
FT   NP_BIND    1075   1082       ATP (POTENTIAL).
FT   CARBOHYD    651    651       N-LINKED (GLCNAC...  .)   (POTENTIAL).
FT   CARBOHYD    690    690       N-LINKED (GLCNAC...  .)   (POTENTIAL).
FT   CARBOHYD    746    746       N-LINKED (GLCNAC...  .)   (POTENTIAL).
FT   CARBOHYD    754    754       N-LINKED (GLCNAC...  .)   (POTENTIAL).
FT   CARBOHYD    792    792       N-LINKED (GLCNAC...  .)   (POTENTIAL).
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FT   CARBOHYD    1176   1176        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    1309   1309        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    1302   1302        H -> D (IN REF. 2).
SQ   SEQUENCE    1325 AA;  149539 MW;  9C5750A748BB96CE CRC64;

Query Match        23.3%;   Score 51;  DB 1;  Length 1325;
Best Local Similarity  40.9%;  Pred. No. 46;
Matches    9;  Conservative   4;  Mismatches   9;  Indels   0;  Gaps   0;

Qy     5 RFGTCTVQKLAHQIYQFTDKDK 26
         :|  :||  :||::   |  ||
Db  1222 KFAHCTVLTIAHRLNTIIDSDK 1243

RESULT 13
G33_RAT
ID   G33_RAT     STANDARD;       PRT;    459 AA.
AC   P05432;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Gene 33 polypeptide.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=89385990; PubMed=2780291;
RA   Chrapkiewicz N.B., Davis C.M., Chu D.T.W., Granner D.K.;
RT   "Rat gene 33: analysis of its structure, messenger RNA and basal
RT   promoter activity.";
RL   Nucleic Acids Res. 17:6651-6667(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX   MEDLINE=89138017; PubMed=3224831;
RA   Tindal M.H., Lee K.L., Isham K.R., Cadilla C., Kenney F.T.;
RT   "Structure of a multihormonally regulated rat gene.";
RL   Gene 71:413-420(1988).
CC   -!- INDUCTION: BY CAMP, GLUCOCORTICOIDS, PHORBOL ESTERS AND
CC       INSULIN.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X07266; CAA30252.1; -.
DR   EMBL; M23572; AAB08828.1; -.
DR   EMBL; M23570; AAB08828.1; JOINED.
DR   EMBL; M23571; AAB08828.1; JOINED.
DR   PIR; S03116; S03116.
SQ   SEQUENCE    459 AA;   49941 MW;  EBD90F11757AC549 CRC64;

Query Match        23.1%;   Score 50.5;  DB 1;  Length 459;
Best Local Similarity  32.4%;  Pred. No. 18;
Matches   11;  Conservative   6;  Mismatches  12;  Indels   5;  Gaps   1;

Qy     5 RFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKISPQ 38
         |:  |:  :|:||  |  ||    ||
Db   262 RISSCT-----HRASPSSDEDKPEIPPRVPIPPR 290

RESULT 14
TYRO_RANNI
ID   TYRO_RANNI  STANDARD;       PRT;    532 AA.
AC   Q04604;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
GN   TYR OR TYRS.
OS   Rana nigromaculata (Japanese pond frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93077054; PubMed=1446833;
RA   Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;
RT   "Cloning and sequencing of the cDNA encoding tyrosinase of the
RT   Japanese pond frog, Rana nigromaculata.";
RL   Gene 121:359-363(1992).
RN   [2]
RP   SEQUENCE OF 1-277 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=95290234; PubMed=7772385;
RA   Miura I., Okumoto H., Makino K., Nakata A., Nishioka M.;
RT   "Analysis of the tyrosinase gene of the Japanese pond frog, Rana
RT   nigromaculata: cloning and nucleotide sequence of the genomic DNA
RT   containing the tyrosinase gene and its flanking regions.";
RL   Jpn. J. Genet. 70:79-82(1995).
CC   -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC       THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC       COMPOUNDS.
CC   -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC       DOPAquinone + H(2)O.
CC   -!- COFACTOR: BINDS TWO COPPER IONS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC   -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC   -----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; D12514; BAA02077.1; -.
DR   EMBL; D37779; BAA07034.1; -.
DR   PIR; JC1392; JC1392.
DR   InterPro; IPR000227; Tyrosinase.
DR   Pfam; PF00264; tyrosinase; 1.
DR   PRINTS; PR00092; TYROSINASE.
DR   PROSITE; PS00497; TYROSINASE_1; 1.
DR   PROSITE; PS00498; TYROSINASE_2; 1.
KW   Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
KW   Transmembrane; Melanin biosynthesis.
FT   SIGNAL         1     19
FT   CHAIN         20    532       TYROSINASE.
FT   DOMAIN        20    475       LUMENAL, MELANOSOME (POTENTIAL).
FT   TRANSMEM     476    499       POTENTIAL.
FT   DOMAIN       500    532       CYTOPLASMIC (POTENTIAL).
FT   METAL        184    184       COPPER A (BY SIMILARITY).
FT   METAL        206    206       COPPER A (BY SIMILARITY).
FT   METAL        215    215       COPPER A (BY SIMILARITY).
FT   METAL        367    367       COPPER B (BY SIMILARITY).
FT   METAL        371    371       COPPER B (BY SIMILARITY).
FT   METAL        394    394       COPPER B (BY SIMILARITY).
FT   CARBOHYD      90     90       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT       10     10       T -> A.
SQ   SEQUENCE    532 AA;   60115 MW;  B27D3080F0C74B3A CRC64;

Query Match        23.1%;   Score 50.5;  DB 1;  Length 532;
Best Local Similarity  34.8%;  Pred. No. 21;
```

```
Matches    16;    Conservative    8;    Mismatches    9;    Indels    13;    Gaps    4;

Qy      4  CRFG----TCTVQK--LAHQIYQFTDKDKD-------NVAPRSKISP  37
           ||||        |!!:: :   |:|: | :||       :|  |  |||
Db    107  CRFGYTGPNCTVRRNMIRKDIFRMTTAEKDKLJAYLNLA-KHTISP 151


RESULT 15
Y4KA_RHISN
ID   Y4KA_RHISN      STANDARD;        PRT;     322 AA.
AC   P55521;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Hypothetical 36.7 kDa protein Y4KA.
GN   Y4KA.
OS   Rhizobium sp. (strain NGR234).
OG   Plasmid sym pNGR234a.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=394;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97305956; PubMed=9163424;
RA   Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA   Perret X.;
RT   "Molecular basis of symbiosis between Rhizobium and legumes.";
RL   Nature 387:394-401(1997).
CC   -!- SIMILARITY: NONE OBVIOUS.
CC   --------------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   .EMBL; AE000081; AAB91733.1; -.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   322 AA;   36690 MW;  177B0AF61FA0C74B CRC64;

Query Match              22.6%;   Score 49.5;  DB 1;  Length 322;
Best Local Similarity    35.3%;   Pred. No. 17;
Matches   12;  Conservative    7;  Mismatches   14;  Indels    1;  Gaps    1;

Qy      7  GTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
           |  |  |||| || ||||| :  | :::: | :
Db    210  GQPKVNKLADEI-QFTTKNSFSATPSAELDPANH 242


Search completed: October 17, 2002, 14:49:12
Job time : 4.39401 secs
```

```
          GenCore version 5.1.3
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```

OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 4.58853 Seconds
                                 (without alignments)
                           837.648 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146
Perfect score: 219
Sequence: 1 SFGCRFGFCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

Scoring table: BLOSUM62
              , Gapop 10.0 , Gapext 0.5

Database :   PIR_71:*
                 1: Pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	219	100.0	185	2	JN0684	adrenomedullin pre
2	213	97.3	188	2	S41600	adrenomedullin - p
3	196	89.5	185	2	JN0766	adrenomedullin pre
4	61.5	28.1	430	2	T14536	S-locus-specific g
5	61	27.9	1541	1	S71839	canalicular multid
6	59	26.9	1545	1	S71841	multidrug resistan
7	58.5	26.7	189	2	A99638	hypothetical prote
8	58.5	26.7	189	2	A85489	hypothetical prote
9	58.5	26.7	431	2	T14415	S-locus-specific g
10	55.5	25.3	428	2	T14529	S-locus-specific g
11	55	25.1	373	2	G84107	lipopolysaccharide
12	54.5	24.9	428	2	T07814	S-locus-specific g
13	54.5	24.9	436	2	A27827	S-locus-specific g
14	53.5	24.4	427	2	T14424	S-locus-specific g
15	53.5	24.4	428	2	T14423	S-locus-specific g
16	53	24.2	465	2	T15540	hypothetical prote
17	52.5	24.0	428	2	T14416	S-locus-specific g
18	52.5	24.0	428	2	T14530	S-locus-specific g
19	52.5	24.0	429	2	T07809	S-receptor kinase
20	51.5	23.5	426	2	T07810	S-locus-specific g
21	51.5	23.5	429	2	T14528	S-locus-specific g
22	51	23.3	93	2	E91004	hypothetical prote
23	51	23.3	93	2	E85637	hypothetical prote
24	51	23.3	319	2	S20799	S-locus-specific g
25	51	23.3	429	2	T14533	hypothetical prote
26	51	23.3	608	2	AD2000	ABC transporter AT
27	51	23.3	759	2	T16368	hypothetical prote
28	51	23.3	857	2	T14471	probable S-recepto
29	50.5	23.1	171	2	D70832	hypothetical prote
30	50.5	23.1	419	2	T27938	hypothetical prote
31	50.5	23.1	459	2	S03116	gene 33 protein, h
32	50.5	23.1	532	2	JC1392	monophenol monooxy
33	50.5	23.1	587	2	S58319	hypothetical prote
34	50.5	23.1	850	2	T14472	S-receptor kinase
35	50.5	23.1	858	1	JQ1677	S-receptor kinase
36	50	22.8	90	2	C86279	hypothetical prote
37	50	22.8	171	2	T51674	myb-related transc
38	50	22.8	250	2	T05996	hypothetical prote
39	50	22.8	1034	2	AB0551	exonuclease SbcC [
40	49.5	22.6	322	2	T47067	hypothetical prote
41	49.5	22.6	356	2	T48354	hypothetical prote
42	49	22.4	204	2	C97389	hypothetical prote
43	49	22.4	204	2	AD2607	conserved hypothet
44	49	22.4	253	2	F90507	sugar phosphate nu
45	49	22.4	431	2	T07812	S-locus-specific g
```

                        ALIGNMENTS

```
RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993.
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A;Reference number: JN0684; MUID:93343928
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A;Reference number: JN0476; MUID:93249425
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match     100.0%;  Score 219;  DB 2;  Length 185;
Best Local Similarity  100.0%;   Pred. No. 8.8e-23;
Matches 40;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
           ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
A;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA enco
A;Reference number: S41600; MUID:94139945
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

Query Match   97.3%; Score 213; DB 2; Length 188;
Best Local Similarity   97.5%; Pred. No. 6.1e-22;
Matches   39; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
           ||||||||||||||||||||||||||||||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
A;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

Query Match   89.5%; Score 196; DB 2; Length 185;
Best Local Similarity   87.5%; Pred. No. 1.4e-19;
Matches   35; Conservative   3; Mismatches   2; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
           ||||||||||||||||||||||||:||::||:||||||||
Db   104 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143

RESULT 4
T14536
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536

R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-430 <KUS>
A;Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   28.1%; Score 61.5; DB 2; Length 430;
Best Local Similarity   28.6%; Pred. No. 1.4;
Matches   14; Conservative   12; Mismatches   12; Indels   11; Gaps   2;

Qy   3 GCRF-GTCTVQKLAHQIYQFTDKDKD--------NVAPRSKISPQGY 40
           || || :||::.:||:.| :   :: .:|||:||
Db   220 GIRFSGIPEDEKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268

RESULT 5
S71839
canalicular multidrug resistance protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
A;Accession: S71839
R;Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler,
J. Biol. Chem. 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan
A;Reference number: S71839; MUID:96279006
A;Accession: S71839
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1541 <BUE>
A;Cross-references: EMBL:X96393; NID:g1292881; PIDN:CAA65257.1; PID:g1617207
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homolo
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;100-124/Domain: transmembrane #status predicted <TM01>
F;127-151/Domain: transmembrane #status predicted <TM02>
F;160-187/Domain: transmembrane #status predicted <TM03>
F;305-329/Domain: transmembrane #status predicted <TM04>
F;354-381/Domain: transmembrane #status predicted <TM05>
F;431-451/Domain: transmembrane #status predicted <TM06>
F;456-476/Domain: transmembrane #status predicted <TM07>
F;536-564/Domain: transmembrane #status predicted <TM08>
F;574-602/Domain: transmembrane #status predicted <TM09>
F;650-833/Domain: ATP-binding cassette homology <ABC1>
F;667-674/Region: nucleotide-binding motif A (P-loop)
F;966-994/Domain: transmembrane #status predicted <TM10>
F;1018-1046/Domain: transmembrane #status predicted <TM11>
F;1104-1132/Domain: transmembrane #status predicted <TM12>
F;1203-1228/Domain: transmembrane #status predicted <TM13>
F;1313-1506/Domain: ATP-binding cassette homology <ABC2>
F;1330-1337/Region: nucleotide-binding motif A (P-loop)
F;6,1007,1010,1011/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   27.9%; Score 61; DB 1; Length 1541;
Best Local Similarity   38.2%; Pred. No. 6.2;
Matches   13; Conservative   4; Mismatches   4; Indels   17; Gaps   0;

Qy   6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 39
           | ||| ||||:::. | || | |
Db   1479 FSQCTVITIAHRLHTIMDSDKIMVLDNGKIVEYG 1512

RESULT 6
S71841
multidrug resistance protein, canalicular - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71841; S71840

R;Koenig, J.; Keppler, D.
submitted to the EMBL Data Library, August 1996
A;Reference number: S71841
A;Accession: S71841
A;Molecule type: mRNA
A;Residues: 1-1545 <KOE>
A;Cross-references: EMBL:X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
R;Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, D.
J. Biol. Chem. 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance
A;Reference number: S71839; MUID:9679006
A;Accession: S71840
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1415-1429,'VP',1432-1455,'E',1457-1545 <BUE>
A;Cross-references: EMBL:X96395
C;Genetics:
A;Gene: GDB:ABCC2; CMOAT; ABC; MRP2; cMRP; DJS
A;Cross-references: GDB:6089489; OMIM:601107
A;Map position: 10q24-10q24
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;654-837/Domain: ATP-binding cassette homology <ABC1>
F;671-678/Region: nucleotide-binding motif A (P-loop)
F;1317-1510/Domain: ATP-binding cassette homology <ABC2>
F;1334-1341/Region: nucleotide-binding motif A (P-loop)

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Query Match         26.9%;  Score 59;  DB 1;  Length 1545;
Best Local Similarity  37.8%;  Pred. No. 12;
Matches  14;  Conservative   5;  Mismatches  14;  Indels   4;  Gaps   1;

Qy     6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
           | ||| :||.:|| ||:::  :||:   |:
Db  1483 FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSPE 1519
```

RESULT 7
A99638
hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
A;Accession: A99638
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:g13359529; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0073
C;Superfamily: Escherichia coli yabP protein

```
Query Match         26.7%;  Score 58.5;  DB 2;  Length 189;
Best Local Similarity  34.4%;  Pred. No. 1.6;
Matches  11;  Conservative   9;  Mismatches   7;  Indels   5;  Gaps   1;

Qy    13 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 39
           || :| :| |      || :|:|:||:|
Db    95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126
```

RESULT 8
A85489
hypothetical protein z0078 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
A;Accession: A85489
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <STO>
A;Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0078
C;Superfamily: Escherichia coli yabP protein

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Query Match         26.7%;  Score 58.5;  DB 2;  Length 189;
Best Local Similarity  34.4%;  Pred. No. 1.6;
Matches  11;  Conservative   9;  Mismatches   7;  Indels   5;  Gaps   1;

Qy    13 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 39
           || :| :| |      || :|:|:||:|
Db    95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126
```

RESULT 9
T14415
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
A;Accession: T14415
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <KUS>
A;Cross-references: EMBL:D85215; NID:g2351161; PIDN:BAA21949.1; PID:g2351162
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

```
Query Match         26.7%;  Score 58.5;  DB 2;  Length 431;
Best Local Similarity  32.7%;  Pred. No. 3.7;
Matches  16;  Conservative   8;  Mismatches  14;  Indels  11;  Gaps   2;

Qy     3 GCRF-GTCTVQKLAHQIYQFTDKDKD--------NVAPRSKISPQGY 40
            :| :|| ::  :|::  | ||: |        :: ||:|:|
Db   222 GVRFSGMPGDQKLNYMVYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270
```

RESULT 10
T14529
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
A;Accession: T14529
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
A;Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

```
Query Match         25.3%;  Score 55.5;  DB 2;  Length 428;
```

Nature 326, 617-619, 1987
A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus
A;Reference number: A93392
A;Accession: A27827
A;Molecule type: mRNA
A;Residues: 1-436 <NAS>
C;Superfamily: S-locus-specific glycoprotein; s-locus-specific glycoprotein homology
C;Keywords: glycoprotein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-436/Product: S-locus-specific glycoprotein S6 #status predicted <MAT>
F;40-434/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match   24.9%; Score 54.5; DB 2; Length 436;
Best Local Similarity   28.6%; Pred. No. 13; Indels 14; Gaps 2;
Matches   15; Conservative   10; Mismatches   14;

Qy   3 GCRF-GTCTVQKLAHQIYQFTDKD-------NVAPRSKISPQGY 40
          | | | | ||||| |||::| || :: : |:|| ||
Db 227 GVRFSGIPEDQKLSYMVYNFTENSEVAYTFRMTNNSIYSRLTLSSEGY 275

RESULT 14
T14424
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14424
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14424
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-427 <KUS>
A;Cross-references: EMBL:D85225; NID:g2351181; PIDN:BAA21959.1; PID:g2351182
C;Superfamily: S-locus-specific glycoprotein; s-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   24.4%; Score 53.5; DB 2; Length 427;
Best Local Similarity   28.6%; Pred. No. 18; Indels 11; Gaps 2;
Matches   14; Conservative   10; Mismatches   14;

Qy   3 GCRF-GTCTVQKLAHQIYQFTDKD-------NVAPRSKISPQGY 40
          | | | | ||||| |||::| || :: : |:|| ||
Db 220 GVRFSGIPEDQKLNYMVYNFTENSEEVAYTFRMTNNSIYSRLKLSSEGF 268

RESULT 15
T14423
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14423
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A;Reference number: Z18078; MUID:97352858
A;Accession: T14423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
A;Cross-references: EMBL:D85223; NID:g2351177; PIDN:BAA21957.1; PID:g2351178
C;Superfamily: S-locus-specific glycoprotein; s-locus-specific glycoprotein homology
C;Keywords: glycoprotein

Query Match   24.4%; Score 53.5; DB 2; Length 428;
Best Local Similarity   28.6%; Pred. No. 18; Indels 11; Gaps 2;
Matches   14; Conservative   10; Mismatches   14;

Best Local Similarity   30.6%; Pred. No. 9.5; Indels 11; Gaps 2;
Matches   15; Conservative   8; Mismatches   15;

Qy   3 GCRF-GTCTVQKLAHQIYQFTDKD-------NVAPRSKISPQGY 40
          | | | | ||||| |||::| || :: : |:|| ||
Db 219 GVRFSGIPENQKLSYMVYNFTENSEEVAYTFRMTNNSFYSRLKVSSDGY 267

RESULT 11
G84107
lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: G84107
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07382.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3663

Query Match   25.1%; Score 55; DB 2; Length 373;
Best Local Similarity   44.8%; Pred. No. 9.7; Indels 0; Gaps 0;
Matches   13; Conservative   4; Mismatches   12;

Qy   7 GTCTVQKLAHQIYQFTDKDKDNVAPRSKI 35
          | ||||| |:| ||| : | ||
Db 128 GFGAVKVKLAHQIVSLSEGVKENLVRRYKI 156

RESULT 12
T07814
S-locus-specific glycoprotein S6 - radish (fragment)
C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07814
R;Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A;Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related gen
A;Reference number: Z16146; MUID:98311079
A;Accession: T07814
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <SAK>
A;Cross-references: EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g3327850
C;Genetics:
A;Gene: SLG(S6)
C;Superfamily: S-locus-specific glycoprotein; s-locus-specific glycoprotein homology <SSG>
C;Keywords: glycoprotein
F;32-426/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match   24.9%; Score 54.5; DB 2; Length 428;
Best Local Similarity   30.6%; Pred. No. 13; Indels 11; Gaps 2;
Matches   15; Conservative   8; Mismatches   15;

Qy   3 GCRF-GTCTVQKLAHQIYQFTDKD-------NVAPRSKISPQGY 40
          | | | | ||||| |||::| || :: : |:|| ||
Db 219 GIRFSGIPEDQKLSYMVYNFTENSEEVAYTFLMTNNSYSRLTISSSGY 267

RESULT 13
A27827
S-locus-specific glycoprotein S6 precursor - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C;Accession: A27827
R;Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.

```
Qy      3  GCRF-GTCTVQKLAHQIYQFTDKD---------NVAPRSKISPQGY  40
           | || |   ||||:: :| || ::       :: | : | :|| :||
Db    218  GIRFSGIPEDQKLSYMVYNFTENSEEVAYTFRLTNSSIYSRLIVSSEGY  266
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Search completed: October 17, 2002, 14:46:17
Job time : 7.58853 secs

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OM protein - protein search, using sw model

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

Run on: October 17, 2002, 14:45:20 ; Search time 9.67581 Seconds
(without alignments)
459.181 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146
Perfect score: 219
Sequence: 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	219	100.0	52	22	AAB75110	Human adrenomedull
2	219	100.0	52	22	AAB91759	Adrenomedullin pep
3	219	100.0	52	22	AAE09818	Human adrenomedull
4	219	100.0	53	22	AAB75111	Glycine extended h
5	219	100.0	53	22	AAB75112	Glycine extended a
6	219	100.0	62	22	AAB75113	Linker peptide-adr
7	219	100.0	120	22	AAB75122	UspA(1-57)-(A)-(GS
8	219	100.0	120	22	AAB75123	UspA(1-56)-(DD)-(G
9	219	100.0	147	22	AAB75124	UspA(1-84)-(A)-(GS
10	219	100.0	170	22	AAB75114	Thioredoxin-(GSGSG
11	219	100.0	185	22	AAB49697	Human adrenomeduli
12	219	100.0	185	22	AAB60344	Human adrenomedull
13	213	97.3	188	22	AAB49698	Porcine adrenomedu
14	213	97.3	188	22	AAB60345	Porcine adrenomedu
15	196	89.5	40	22	AAB91768	Adrenomedullin pep
16	196	89.5	50	22	AAE09819	Rat adrenomedullin
17	196	89.5	185	22	AAB49699	Rat adrenomedullin
18	196	89.5	185	22	AAB60346	Rat adrenomedullin
19	184.5	84.2	53	22	AAB91767	Adrenomedullin pep
20	181.5	82.9	37	22	AAB91761	Adrenomedullin pep
21	179.5	82.0	52	22	AAB91765	Adrenomedullin pep
22	163	74.4	31	18	AAW25160	Human preproadreno
23	163	74.4	31	22	AAB91762	Adrenomedullin pep
24	163	74.4	31	22	AAE09827	Human adrenomedull
25	61	27.9	1541	18	AAW33361	Rat canalicular mu
26	60	27.4	231	21	AAB11449	Human CMOAT C-term
27	60	27.4	231	21	AAB28224	Multi-drug resista
28	60	27.4	1545	18	AAW33362	Human canalicular
29	59	26.9	1545	19	AAW55966	Human canalicular
30	57	26.0	13	18	AAW25159	Human preproadreno
31	56	25.6	1302	22	ABB65954	Drosophila melanog
32	55	25.1	1344	22	ABB59224	Drosophila melanog
33	54	24.7	1327	22	ABB63391	Drosophila melanog
34	54	24.7	1346	22	ABB65953	Drosophila melanog
35	53.5	24.4	436	19	AAW56306	Clas I S-locus gly
36	53.5	24.4	846	19	AAW56307	Clas I S-receptor
37	53	24.2	892	22	ABB62270	Drosophila melanog
38	53	24.2	1348	22	ABB60761	Drosophila melanog
39	52	23.7	229	22	ABG05415	Novel human diagno
40	52	23.7	229	22	ABG13273	Novel human diagno
41	52	23.7	677	22	ABG09129	Novel human diagno
42	52	23.7	775	19	AAW58582	Kojibiose phosphor
43	52	23.7	939	22	ABG14932	Novel human diagno
44	52	23.7	994	22	ABG10411	Novel human diagno
45	52	23.7	1547	22	ABB66152	Drosophila melanog

ALIGNMENTS

RESULT 1
AAB75110
ID   AAB75110 standard; Protein; 52 AA.
XX
AC   AAB75110;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Human adrenomedullin (AM) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;   99JP-0294147.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19806.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX

PS   Disclosure; Page 45; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   52 AA;

Query Match   100.0%;   Score 219; DB 22;   Length 52;
Best Local Similarity   100.0%; Pred. No. 2.5e-24;
Matches 40: Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        ||||||||||||||||||||||||||||||||||||||||
Db 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 2
AAB91759
ID   AAB91759 standard; Peptide; 52 AA.
XX
AC   AAB91759;
XX
DT   22-JUN-2001 (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
-
XX
PS   Disclosure; Page 498; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase therapeutic
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.

CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   52 AA;

Query Match   100.0%;   Score 219; DB 22;   Length 52;
Best Local Similarity   100.0%; Pred. No. 2.5e-24;
Matches 40: Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        ||||||||||||||||||||||||||||||||||||||||
Db 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 3
AAE09818
ID   AAE09818 standard; peptide; 52 AA.
XX
AC   AAE09818;
XX
DT   29-NOV-2001 (first entry)
XX
DE   Human adrenomedullin peptide #1.
XX
KW   Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW   CGRP-receptor identification; adrenomedullin.
XX
OS   Homo sapiens.
XX
PN   US6268474-B1.
XX
PD   31-JUL-2001.
XX
PF   30-APR-1998;   98US-0070504.
XX
PR   30-APR-1998;   98US-0070504.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Smith DD, Saha S, Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related
PT   peptide receptor activity -
XX
PS   Claim 5; Column 25-26; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide
CC   calcitonin gene related peptide (CGRP) and other members of the
CC   CGRP superfamily. The invention also relates to amino the terminal
CC   modifications of peptides to improve their ability to bind to a
CC   member of the CGRP-receptor super-family. CGRP antagonists are
CC   used for inhibiting CGRP activity which can be used in vitro e.g.
CC   in assays to identify and/or isolate CGRP receptors or with intact
CC   cells either in vitro or in vivo to inhibit the effect of CGRP
CC   binding to its receptor. The present sequence is human
CC   adrenomedullin peptide.
XX
SQ   Sequence   52 AA;

Query Match   100.0%;   Score 219; DB 22;   Length 52;
Best Local Similarity   100.0%; Pred. No. 2.5e-24;
Matches 40: Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
        ||||||||||||||||||||||||||||||||||||||||
Db 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

```
RESULT 4
AAB75111
ID   AAB75111 standard; Protein; 53 AA.
XX
AC   AAB75111;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Glycine extended human adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19807.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Example 1; Page 46; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   53 AA;

Query Match             100.0%;    Score 219;  DB 22;    Length 53;
Best Local Similarity   100.0%;    Pred. No. 2.6e-24;
Matches   40;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||||||||||||||||||||||||
Db   13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 5
AAB75112
ID   AAB75112 standard; Protein; 53 AA.
XX
AC   AAB75112;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Glycine extended adrenomedullin (AM-gly) protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19808.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Disclosure; Page 47; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   53 AA;

Query Match             100.0%;    Score 219;  DB 22;    Length 53;
Best Local Similarity   100.0%;    Pred. No. 2.6e-24;
Matches   40;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||||||||||||||||||||||||
Db   13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 6
AAB75113
ID   AAB75113 standard; Protein; 62 AA.
XX
AC   AAB75113;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Linker peptide-adrenomedullin (AM) precursor protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19809.
```

```
XX
PT  Producing adrenomedullin useful for pharmaceutical and diagnostic
PT  application comprises producing fused adrenomedullin precursor using a
PT  recombinant host -
XX
PS  Claim 20; Page 48; 75pp; Japanese.
XX
CC  The present invention describes a method (M1) for producing
CC  adrenomedullin precursor. The method comprises: (a) producing the fused
CC  protein using a recombinant host cell; (b) restricted digestion of the
CC  fused protein by a protease followed by collection of sediment; and
CC  (c) dissolving the sediment and extracting adrenomedullin precursor.
CC  The method can be used for the production of adrenomedullin precursor.
CC  for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC  and AAB75110 to AAB75124 represent sequences which are used in the
CC  exemplification of the present invention.
XX
SQ  Sequence  62 AA;

Query Match           100.0%;   Score 219;  DB 22;  Length 62;
Best Local Similarity 100.0%;   Pred. No. 3.1e-24;
Matches  40;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
       ||||||||||||||||||||||||||||||||||||||||
Db  22 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 61

RESULT 7
AAB75122
ID  AAB75122 standard; Protein; 120 AA.
XX
AC  AAB75122;
XX
DT  31-JUL-2001  (first entry)
XX
DE  UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW  adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200127310-A1.
XX
PD  19-APR-2001.
XX
PF  10-OCT-2000; 2000WO-JP07023.
XX
PR  15-OCT-1999;  99JP-0294147.
XX
PA  (SHIO ) SHIONOGI & CO LTD.
XX
PI  Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR  WPI; 2001-282044/29.
DR  N-PSDB; AAH19864.
XX
PT  Producing adrenomedullin useful for pharmaceutical and diagnostic
PT  application comprises producing fused adrenomedullin precursor using a
PT  recombinant host -
XX
PS  Claim 17; Page 68; 75pp; Japanese.
XX
CC  The present invention describes a method (M1) for producing
CC  adrenomedullin precursor. The method comprises: (a) producing the fused
CC  protein using a recombinant host cell; (b) restricted digestion of the
CC  fused protein by a protease followed by collection of sediment; and
CC  (c) dissolving the sediment and extracting adrenomedullin precursor.
CC  The method can be used for the production of adrenomedullin precursor.
CC  for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC  and AAB75110 to AAB75124 represent sequences which are used in the
CC  exemplification of the present invention.
XX
SQ  Sequence  120 AA;

Query Match           100.0%;   Score 219;  DB 22;  Length 120;
Best Local Similarity 100.0%;   Pred. No. 6.6e-24;
Matches  40;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
       ||||||||||||||||||||||||||||||||||||||||
Db  80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119

RESULT 8
AAB75123
ID  AAB75123 standard; Protein; 120 AA.
XX
AC  AAB75123;
XX
DT  31-JUL-2001  (first entry)
XX
DE  UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
XX
KW  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW  adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200127310-A1.
XX
PD  19-APR-2001.
XX
PF  10-OCT-2000; 2000WO-JP07023.
XX
PR  15-OCT-1999;  99JP-0294147.
XX
PA  (SHIO ) SHIONOGI & CO LTD.
XX
PI  Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR  WPI; 2001-282044/29.
DR  N-PSDB; AAH19865.
XX
PT  Producing adrenomedullin useful for pharmaceutical and diagnostic
PT  application comprises producing fused adrenomedullin precursor using a
PT  recombinant host -
XX
PS  Claim 17; Page 69-70; 75pp; Japanese.
XX
CC  The present invention describes a method (M1) for producing
CC  adrenomedullin precursor. The method comprises: (a) producing the fused
CC  protein using a recombinant host cell; (b) restricted digestion of the
CC  fused protein by a protease followed by collection of sediment; and
CC  (c) dissolving the sediment and extracting adrenomedullin precursor.
CC  The method can be used for the production of adrenomedullin precursor
CC  for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC  and AAB75110 to AAB75124 represent sequences which are used in the
CC  exemplification of the present invention.
XX
SQ  Sequence  120 AA;

Query Match           100.0%;   Score 219;  DB 22;  Length 120;
Best Local Similarity 100.0%;   Pred. No. 6.6e-24;
Matches  40;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
       ||||||||||||||||||||||||||||||||||||||||
Db  80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119

RESULT 9
AAB75124
```

```
ID   AAB75124 standard; Protein; 147 AA.
XX
AC   AAB75124;
XX
DT   31-JUL-2001  (first entry)
XX
DE   UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19866.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 71; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  147 AA;

Query Match             100.0%;  Score 219;  DB 22;  Length 147;
Best Local Similarity   100.0%;  Pred. No. 8.3e-24;
Matches  40;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         ||||||||||||||||||||||||||||||||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146

RESULT 10
AAB75114
ID   AAB75114 standard; Protein; 170 AA.
XX
AC   AAB75114;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Thioredoxin-(GSGSGDAFE)-AM-gly protein.
XX
KW   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW   adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200127310-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-JP07023.
XX
PR   15-OCT-1999;  99JP-0294147.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR   WPI; 2001-282044/29.
DR   N-PSDB; AAH19810.
XX
PT   Producing adrenomedullin useful for pharmaceutical and diagnostic
PT   application comprises producing fused adrenomedullin precursor using a
PT   recombinant host -
XX
PS   Claim 17; Page 49-50; 75pp; Japanese.
XX
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and
CC   (c) dissolving the sediment and extracting adrenomedullin precursor.
CC   The method can be used for the production of adrenomedullin precursor
CC   for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC   and AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention.
XX
SQ   Sequence  170 AA;

Query Match             100.0%;  Score 219;  DB 22;  Length 170;
Best Local Similarity   100.0%;  Pred. No. 9.8e-24;
Matches  40;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         ||||||||||||||||||||||||||||||||||||||||
Db  130 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169

RESULT 11
AAB49697
ID   AAB49697 standard; Protein; 185 AA.
XX
AC   AAB49697;
XX
DT   04-APR-2001  (first entry)
XX
DE   Human adrenomedullin amino acid sequence.
XX
KW   Passive elongation; vesicle smooth muscle; uropathic activity;
KW   adrenomedullin; urinary disorder; incontinence; human.
XX
OS   Homo sapiens.
XX
PN   WO20007838-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04166.
XX
PR   23-JUN-1999;  99JP-0177549.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080754/09.
DR   N-PSDB; AAF29138.
XX
PT   Composition for promoting passive elongation of vesicle smooth muscle
PT   comprises adrenomedullin -
```

XX
PS Claim 1; Page 26-27; 42pp; Japanese.
XX
CC This invention relates to a composition for promoting passive elongation
CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC uropathic activity. The composition can be used for promoting passive
CC elongation of vesicle smooth muscles, this is useful for relieving
CC urinary disorders such as impending urinary incontinence, reflex urinary
CC incontinence and urinary incontinence with overflow. The present sequence
CC represents the human adrenomedullin protein, which is used in the
CC composition of the invention.
XX
SQ Sequence 185 AA;

Query Match   100.0%;   Score 219;   DB 22;   Length 185;
Best Local Similarity   100.0%;   Pred. No. 1.1e-23;
Matches   40;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||||||||||||||||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
```

RESULT 12
AAB60344
ID AAB60344 standard; Protein; 185 AA.
XX
AC AAB60344;
XX
DT 06-APR-2001 (first entry)
XX
DE Human adrenomedullin precursor.
XX
KW Human; adrenomedullin; precursor; bradykinin antagonist;
KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW dysmenorrhoea; obstetric; gynaecological.
XX
OS Homo sapiens.
XX
PN WO200078339-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04167.
XX
PR 23-JUN-1999; 99JP-0177548.
PR 21-MAR-2000; 2000JP-0079171.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Yanagita T;
XX
DR WPI; 2001-080755/09.
DR N-PSDB; AAF27228.
XX
PT Composition for inhibiting automatic uterine contraction or contraction
PT caused by bradykinin comprises adrenomedullin -
XX
PS Claim 7; Page 37-38; 54pp; Japanese.
XX
CC The invention relates to a composition containing adrenomedullin for
CC inhibiting automatic uterine contraction or contraction caused by
CC bradykinin. The invention also relates to the use of adrenomedullin in
CC the preparation of a drug for preventing premature birth or miscarriage.
CC The composition of the invention can be used for preventing premature
CC birth, preventing miscarriage, stopping delivery before caesarean
CC section or for treating dysmenorrhoea. The present sequence
CC represents human adrenomedullin precursor.
XX
SQ Sequence 185 AA;

Query Match   100.0%;   Score 219;   DB 22;   Length 185;
Best Local Similarity   100.0%;   Pred. No. 1.1e-23;
Matches   40;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          ||||||||||||||||||||||||||||||||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
```

RESULT 13
AAB49698
ID AAB49698 standard; Protein; 188 AA.
XX
AC AAB49698;
XX
DT 04-APR-2001 (first entry)
XX
DE Porcine adrenomedullin amino acid sequence.
XX
KW Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; procine.
XX
OS Sus scrofa.
XX
PN WO200078338-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04166.
XX
PR 23-JUN-1999; 99JP-0177549.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Yanagita T;
XX
DR WPI; 2001-080754/09.
DR N-PSDB; AAF29139.
XX
PT Composition for promoting passive elongation of vesicle smooth muscle
PT comprises adrenomedullin -
XX
PS Disclosure; Page 31-33; 42pp; Japanese.
XX
CC This invention relates to a composition for promoting passive elongation
CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC uropathic activity. The composition can be used for promoting passive
CC elongation of vesicle smooth muscles, this is useful for relieving urinary
CC urinary disorders such as impending urinary incontinence, reflex urinary
CC incontinence and urinary incontinence with overflow. The present sequence
CC represents the porcine adrenomedullin protein, which is used in the
CC composition of the invention.
XX
SQ Sequence 188 AA;

Query Match   97.3%;   Score 213;   DB 22;   Length 188;
Best Local Similarity   97.5%;   Pred. No. 8.2e-23;
Matches   39;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   0;

```
Qy    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
          |||||||||||||||||||||||||||| |||||||||||
Db  107 SFGCRFGTCTVQKLAHQIYQFTDKDGVAPRSKISPQGY 146
```

RESULT 14
AAB60345
ID AAB60345 standard; Protein; 188 AA.
XX
AC AAB60345;
XX
DT 06-APR-2001 (first entry)
XX
DE Porcine adrenomedullin precursor.
XX
KW Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;

KW   uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW   dysmenorrhoea; obstetric; gynaecological.
XX
OS   Sus scrofa.
XX
PN   WO200078339-A1.
XX
PD   28-DEC-2000.
XX
PF   23-JUN-2000; 2000WO-JP04167.
XX
PR   23-JUN-1999; 99JP-0177548.
PR   21-MAR-2000; 2000JP-0079171.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Yanagita T;
XX
DR   WPI; 2001-080755/09.
DR   N-PSDB; AAF27229.
XX
PT   Composition for inhibiting automatic uterine contraction or contraction
PT   caused by bradykinin comprises adrenomedullin -
XX
PS   Disclosure: Page 43-44; 54pp; Japanese.
XX
CC   The invention relates to a composition containing adrenomedullin for
CC   inhibiting automatic uterine contraction or contraction caused by
CC   bradykinin. The invention also relates to the use of adrenomedullin in
CC   the preparation of a drug for preventing premature birth or miscarriage.
CC   The composition of the invention can be used for preventing premature
CC   birth, preventing miscarriage, stopping delivery before caesarean
CC   section or for treating dysmenorrhoea. The present sequence
CC   represents porcine adrenomedullin precursor.
XX
SQ   Sequence 188 AA;

Query Match   97.3%; Score 213; DB 22; Length 188;
Best Local Similarity   97.5%; Pred. No. 8.2e-23;
Matches   39; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
           ||||||||||||||||||||||||||| ||||||||||||
Db   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146

RESULT 15
AAB91768
ID   AAB91768 standard; Peptide; 40 AA.
XX
AC   AAB91768;
XX
DT   22-JUN-2001 (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:944.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999; 99US-0134406.
PR   10-SEP-1999; 99US-0153406.
PR   15-OCT-1999; 99US-0159783.
XX

PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure: Page 502; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracelular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 40 AA;

Query Match   89.5%; Score 196; DB 22; Length 40;
Best Local Similarity   87.5%; Pred. No. 4e-21;
Matches   35; Conservative   3; Mismatches   2; Indels   0; Gaps   0;

Qy   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
         |||||||| ||||||||||||||||||| :||:|||||||
Db   1 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 40

Search completed: October 17, 2002, 14:47:59
Job time : 11.6758 secs